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> *CtManS* -1964 bp.

GGAATTCGGCACGAGGTGCC TGCAACAAGTCAC TAGTCCATCC TGCAGTTCCTAACCCT
CCCTAGTGTCTTTCTCTTCAGGCTCCATATTCCTTTATAACTACTACAATAGATACAATG
AGAAACCTAATCTTCGAGGAGCCTGAAGGGATTCCAGGCAACAGTTCAAGCAGTCTGCGC
TATGCC TGGCAATCAATTCGTGCCCCAGTGATCATACTCTTCTAAAAC TAGCAGTCATA
GTGTGCTCAGTTATGTCAATCATGCTATTTGTTGAAAGAGTAGCCATGGCAGCTGTAATT
TTGATTGTCAAAGTGCTGAGGAAGAAAAGATACACCAAGTATAACTTGGGAAGCCATGAAA
CAGAAGCTAGAGAGAAGCAAAAAATACCCCATGGTGCTGATCCAAATACCTATGTATAAC
GAGAAAGAGGTGTACAAGCTTTCCATTGGAGCAGTATGTGGGCTTTTCATGGCCAGCTGAC
AGGTTTCATAGTTCAAAGTTCTTGATGACTCAACAAATCCAGTCTTAAGGGAGTTGGTTGAA
ATGGAGTGTCAAAAATGGATACAGAAAGGTGTGAATGTCAAGTATGAAAATAGGAGAAAT
CGCAATGGTTACAAAGCAGGTGCC TTAAGAGGGTTTGGAGAAGCAATATGTAGAGGAT
TGTGAGTTTGTAGCAATATTTGATGCAGATTTCCAACCAGATGCGGATTTTCTTTGGAAC
ACAATTCCTTATCTGCTGGA AAAATCCAAAGTTGGGTTTGGTTCAGGCGAGATGGAAATTT
GTGAAC TCAGAAGAATGTATGATGACACGGCTTCAAGAGATGTCAC TAGATTACCACTTT
AGTGT TGAACAGGAAGTCGGCTCTTCAACATACTCATTTCTTCGGTTTCAATGGAACAGCA
GGAGTTTGGCGGATCCAAGCCATAAAAGATGCTGGAGGATGGAAAGACCGAACAACGGTG
GAGGATATGGACCTTGCAGTTAGAGCAAGCTTGCATGGCTGGGAATTTGTTTTTGTGGGT
GATGTAAAGGTCAAAAATGAATTACCAAGTACATTTAAAGCATATCGATTTTCAGCAGCAC
AGGTGGTCATGCGGTCCAGCTAATCTCTTTAAGAAAATGACCAAGGAAATCATCTGTTGC
AAAAGGGTGCCACTTCTCAAGAGACTCCATCTCATCTATGCTTTCTTCTTTGTGAGAAA
ATAGTTGCACACTGGGTTACGTTCTTCTTTTACTGCATAGTTATACCAGCTTGTGTGATA
GTTCCCGAAGTTAATCTCAAAAAGCAGATTGCCATATACATCCCAGCAACCATTACAATT
CTAAATGCAGTCTCCACCCCAAGATCCATGCATCTACTAGTACTCTGGATACTCTTTGAG
AATGTCATGTCACTCCATCGAACTAAAGCAGCAATTATTGGACTCTTGGGAAGCAAATCGT
GTCAATGAATGGGTTGTGACTGAGAAGCTTGGAAATGCCATGAAACAGAGGAACAATGCT
AGGCCATCAAGAGCTTACGGTTTTCGAATTATAGAAAGGATCCACCCATTGGAGATTATA
GTGGGGATGTATATGCTGCACTGTGCAACCTATGACCTGTTATTTCGGACACGACCATTTCT
TTTGTCTATCTTCTGTTGCAGGCAGGGGCGTTCTTTACAATGGGATTTGGCCTAGTAGGA
ACAATTGTACCCACCTAAAGCTTAAAGGTCATGGACTCATGAACATAAGTATTAGTGTAT
GAACGGGTCCCTGTTTGTTTTAAGACTCTAAGTCTAGTGAAC TAGCTATCCATAAGCATAG
AAGTGTAAAGAGAAGCTACGGCTACTTAGTAGAAGCATTCCATATGGTATCAGGACTTCTT
TGTACCCATGTATAAGAACCAGAATCAAAACGTATAAACATGTCCATAATATGAAGCTTA
AATAAATCTGTTATCTGCAC TAAAAAAAAAAAAAAAAAAAAAAC

FIGURE 1

>CiMANS - 526 aa.

MRNLIFEEPEGIPGNSSSSRLRYAWQSIRAPVIIPLLKLAVIVCSVMSIMLFVERVAMAAV
ILIVKVLRRKKRYTKYNLEAMKQKLEERSKKYPMVLIQIPMYNEKEVYKLSIGAVCGLSWPA
DRFIVQVLDDSTNPVLRRELVEMECQKWIQKGVNVKYENRRNRNGYKAGALKEGLEKQYVE
DCEFVAIFDADFQPDADFLWNTIPYLLENPKLGLVQARWKFNSEECMMTRLQEMSLDYH
FSVEQEVGSSTYSFFGFNGTAGVWRIQAIKDAGGWKDRTTVEDMDLAVRASLHGWEFVFV
GDVKVKNELPSTFKAYRFQQHRWSCGPANLFKKMTKEIICCKRVPLLKRLHLIYAFFFVR
KIVAHWVTFFFYCIVIPACVIVPEVNLKKQIAIYIPATITILNAVSTPRSMHLLVLWILF
ENVMSLHRTKAAIIGLLEANRVNEWVTEKLGNAMKQRNNARPSRASRFRIIERIHPLEI
IVGMYMLHCATYDLLFGHDHFFVYLLLQAGAFFTMGFGLVGTIVPT

FIGURE 2

>*CtGalT2* - 1609 bp.

GGAATTTCGGCACGAGGCTCCCATGGCGAAATCCTCCAATTCCAGAAACAAAATTTACACAC
GTAAACCTCTCCGACGGTTTCCTCTTCCTCGCCGGAGCATTCTCCGCGCTTCTAATCGTT
TGGGGTTTCTCCTCCTTCACAACCCCCATCCCTAACGAAACCCCAACCTTCGAATCACTT
TCGGTAAATTCTCACC AAAACGACGCCGTTCGCGCGGGGGACCGGATTTCCGGTTTCGAT
CCCCCGGACCGGACTTCTACGACGACCCGGAATGGGGTACACCATAGACACGACGGTG
CGAGATTGGGATGCAAAGCGTGAGGAGTGGCTGCGGCTTCATCCTTCTTCGCCGCCGGA
GCGAGAGAACGAGTTTTGGTGGTGACCGGATCGCAGCCGGCACC GTGCCGGAATCCCATC
GGCGACCACTTGCTGTTACGGTTTTTTAAGAACAAGGTGGATTACTGTTCGGTTACACGGG
TACGATATCGTGTAACAATGCATTGTTACACCCGAAAATGTTTACGTATTGGGCGAAG
TACCCGGTGGTGCGGGCCGCGATGATGGCCCAACCGGAAGCCGAGTGGATCTGGTGGGTC
GACTCGGACGCGTTGTTACCCGACATGGAGTTCAAAC TACCATTAGATCACTACAAGGAT
CACAACCTCGTCGTCCATGGCTGGGCCCACCTCATCCACGAGAAACGTAGTTGGACGGGC
CTCAACGCCGGCGTCTTCCTCATCAGAAACTGTCAATGGTCATTGGACTTCATAAACGAA
TGGGCCAGCATGGGCCCACAACTCCGAAC TACGAGAAATGGGGTCAAACCTTAAAGTCA
ACTTTCAAAGACAAATTCCTCCCGGAGTCAGACGATCAGACGGGCCTCGCTTACCTGATC
GCGATCGAGAAAGAAAAATGGGCGGACAAGATTTACTTAGAGAACTCGTATTATTTCGAA
GGGTACTGGGAAGAAATCGTCGGAACATTCGAGAATATAAGCAAGAAATACAACGAGATC
GAAACGGGGGTGCGCAGGTTAAGAAGGCGTCACGCGGAGAAAGTGAGTGAAGCTTACGGT
GAAGAGAGGGGAGAAATATTTAACGGAAGCAGGTAACGGTAAAGGAAGCTGGAGACGGCCG
TTTGTGACGCAC TTCACGGGGTGTCAACCTTG TAGCGGAAAATATAACGCTATGTATAAC
GCCGAAGATTGTTGGAACGGAATGCGTAAAGCCCTTAATTTTCGCTGATAATCAGGTGATG
CGTAAATATGGTTTCGTACACCCGGATGTACTAGATAATTCCGTTTCGCCGATTCCGTTT
GATTATCCCCGTAACCGCTCAGGTAATAATCATATTTAATGGAATCTAATTATTGTTGAC
CGCTGGCTACTCAGATTCTCCATGTGTTCTGTAAAGTACTAGTACTACTAGTATTAAATT
TCTTAGTGTATATTTTATAATATTTTATTGTATATTTCTGGCGTTTTGCATATATAGT
ATCGTGTGGAGTAGTATTTAATTATGCATAAGTGAAGGGATAATTTTATTCTTTTCGAAT
CCCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACT

FIGURE 3

>CiGALT2 - 445 aa.

MAKSSNSRNKISHVNLSDGFLFLAGAFSAFLIVWGFSSFTTPIPNETPTFESLSVNSHQN
DAVSRGGPDFRFDPPDRTFYDDPEMGYTIDTTVRDWDAKREEWRLRHPSFAAGARERVLV
VTGSQPAPCRNPIGDHLLLRFFKNKVDYCRLHGYDIVYNNALLHPKMFTYWAKYPVVRAA
MMAHPEAEWIWWVDSALFTDMEVXLPLDHYKDHNLVVHGWAHLIHEKRSWTGLNAGVFL
IRNCQWSLDFINEWASMGPTPNYEKGQTLKSTFKDKFFPESDDQTGLAYLIAIEKEKW
ADKIYLENSYYFEGYWEEIVGTFENISKYNEIETGVRRLRRRHAEKVSEAYGEEREKYL
TEAGNGKGSWRRPFVTHFTGCQPCSGKYNAMYNAEDCWNGMRKALNFADNQVMRKYGFVH
PDVLDNSVSPIPFDYPRNRSGNNHI

FIGURE 4

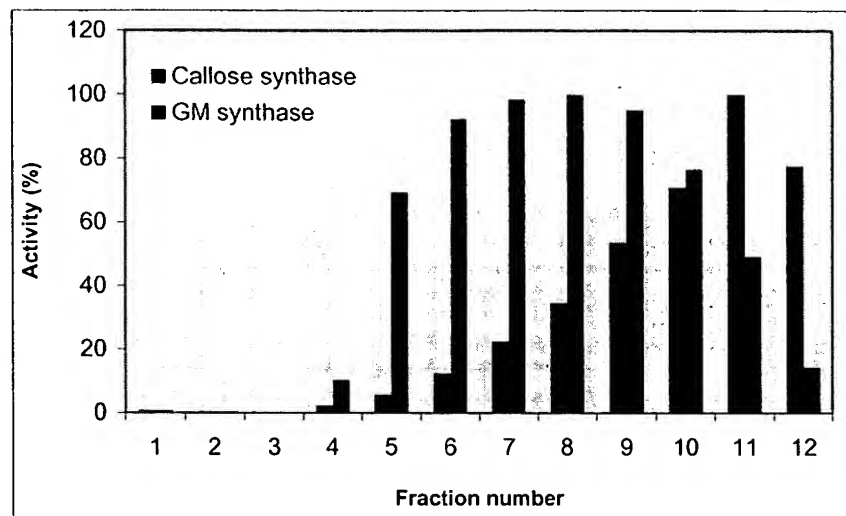


FIGURE 5

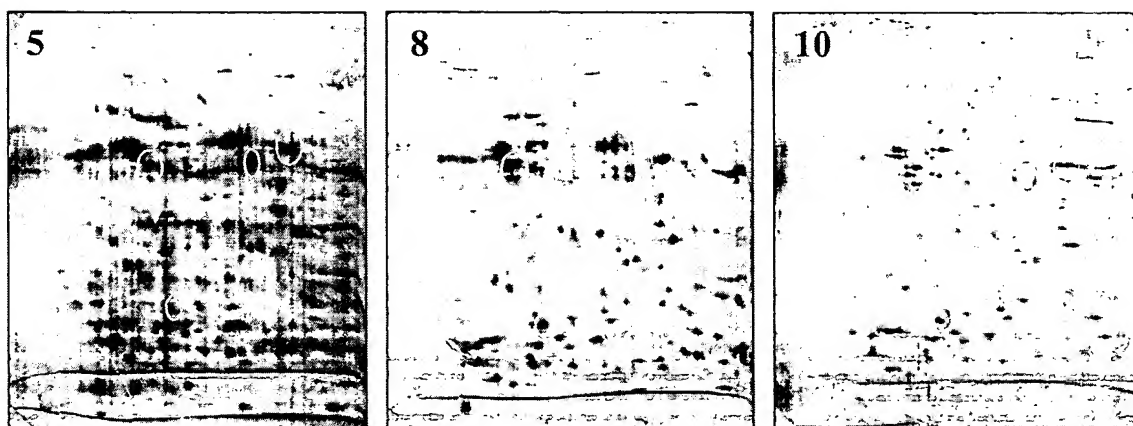


FIGURE 6

| | | | |
|------------|-------|--|-----|
| | | 1 | 60 |
| Fenugreek | (1) | -----GCGACGAAATTGG----- | |
| Guar-GalT1 | (1) | GGAAATTCGGCAGGAGCTCCAGTATCAATTCACTCACTCCCATGGCCAAATTGG----- | |
| Guar-GalT2 | (1) | -----GGAATTGGCAGGAGCTCCCATGGCGAAATCTCCAAT----- | |
| Consensus | (1) | G A C CTCCCATGGCGAAATTGG T | |
| | | 61 | 120 |
| Fenugreek | (16) | TCCRAAAACAAATCCTCTCC--ATGGCTCTCAAATGGTTGCATCTTCTCTCTAGGTGCA | |
| Guar-GalT1 | (58) | TCCAGAAACAAATCCTCTAA--ATGGATCTCCAACGGTTGCTGCTTCTCTCTAGGAGCA | |
| Guar-GalT2 | (40) | TCCAGAAACAAATTTACACGTAACCTCTCCGACGGTTTCTCTTCTCTGCGCGAGCA | |
| Consensus | (61) | TCCAGAAACAAATCCTCTCA ATGGCTCTCCAACGGTTGC TCTTCTCTCTAGGAGCA | |
| | | 121 | 180 |
| Fenugreek | (73) | ATGTCAGCTCTTCTTATGATTTGGGGGCTCAATTCCTTCATCGCTCCAATCCCAAACTCC | |
| Guar-GalT1 | (115) | TTCACTGCTCTTCTTCTGCTCTGGGGTTTATGCTCCTTCATCATCCCCATCCCAAAACCC | |
| Guar-GalT2 | (100) | TTCTCCGCGCTTCTAATCGTTTGGGGTTTCTCTCTCTCAACACCCCATCCCTAACGAA | |
| Consensus | (121) | TTCTC GCTCTTCTTATG TTTGGGGTTTCT CTCCTTCATCACCCCATCCCAAAAC CC | |
| | | 181 | 240 |
| Fenugreek | (133) | AACCCAAATTCAACTCGTTGACCACCAAACTCAAATCCTTAAACTTCACCACAAACACG | |
| Guar-GalT1 | (175) | GACCCCAAGCTCAACTCCGTCGCCACCACTTTGAGATCCCTTAACCTTCCCAAAACCCG | |
| Guar-GalT2 | (160) | ACCCCAACCTTCGAATCACT-----TCGGTAAATTCCTCAACCAAAACGAC | |
| Consensus | (181) | AACCCAAA TTCAACTCC TC CCACCA T T A ATCC TAAACTTTCCCAAAAC CC | |
| | | 241 | 300 |
| Fenugreek | (193) | A----AC-TTTGCTGGTCTGATTTGTACATGACCCCTTCAGACAAACCTTCTATGAT | |
| Guar-GalT1 | (235) | GCTGCCAC-CITGCC--TCCCACTTGGAGCAGCACCCCTCCTGACACACCTTCTACGAC | |
| Guar-GalT2 | (205) | GCGTTTTCGGCGGGGACCGGATTTCCGGTTGGATCCCGGACCGGACTTCTACGAC | |
| Consensus | (241) | GC G AC CTTC GGTCC GATTTGC GCACGACCTCC GACA ACCTTCTACGAC | |
| | | 301 | 360 |
| Fenugreek | (247) | GATCCAGAAACATGTTACACCATGATGGACAAACCAATGAAAAATTGGGATGAGAAGCGT | |
| Guar-GalT1 | (292) | GACCCGAAACAGTTATACCAT---GGACAAACCAATGAAAAACTGGGACGAGAAGCGT | |
| Guar-GalT2 | (265) | GACCCGAAATGGGGTACACCAT---AGACACGACGGTCCGAGATTGGGATGCAAGCGT | |
| Consensus | (301) | GACCC GAAAC GTTACACCAT GGACAAACCAATGAAAAATTGGGATGAGAAGCGT | |
| | | 361 | 420 |
| Fenugreek | (307) | AAAGATGGCTATTTTCATCATCCCTCATTCGCGGCTGGAGCAACCGAAAAGATACTGTG | |
| Guar-GalT1 | (349) | AAGGAGTGGTTGCTGCATCATCTTCTGTTTGGCGCCGACGACGCGATAAGATTCTCCTG | |
| Guar-GalT2 | (322) | GAGGAGTGGCTGCGGCTTCATCTTCTCTCGCGCCGGAGCGAGAGACGAGTTTGGTG | |
| Consensus | (361) | AAGGAGTGGCTGCTGCATCATCTTC TTCGCGCCGGAGCAAGCGAAAAGATTCT GTG | |
| | | 421 | 480 |
| Fenugreek | (367) | ATAACGGGTTACAGCCGACAAAGTGTGCAACCCCATCGGAGACCACCTTTTACTAAGG | |
| Guar-GalT1 | (409) | GTGACAGGTTCTCAGCCGAAACGGTGCCATAACCCGATCGGCGACCACTCTGTGTGGG | |
| Guar-GalT2 | (382) | GTGACCGGATCGCAGCCGACCGTGCCGGAATCCCATCGGCGACCACTTGTGTTACCG | |
| Consensus | (421) | GTGAC GGTTC CAGCCGACAC GTGCCA AACCCCATCGGCGACCACT CTGTTACGG | |
| | | 481 | 540 |
| Fenugreek | (427) | TTCTATAAAACAAGGTGATTATTGTCGTATACACAACACGACATAATCTACAACAAT | |
| Guar-GalT1 | (469) | TTTTCAAGAACAAAGGTGGATTACTGCGGGCTGCACAACTACGACATAATTTACAACAAC | |
| Guar-GalT2 | (442) | TTTTTTAAGAACAAAGGTGGATTACTGTGCGGTACACGGGTACGATATCGTGTACAACAAT | |
| Consensus | (481) | TTTTTTAAGAACAAAGGTGGATTACTGTGCG TACACAACCTACGACATAAT TACAACAAT | |
| | | 541 | 600 |
| Fenugreek | (487) | GCATTGTTGCACCCAAAATGGACTCTTACTGGGCCAAGTATCCTATGGTTCCGGCCGCA | |
| Guar-GalT1 | (529) | GCGCTTCTGCATCCTAAAATGAACCTCTTATGGGCCAAGTATCCAGTGATTCCGGCGGCG | |
| Guar-GalT2 | (502) | GCATTGTTACACCCGAAAATGTTACGTTATTGGGCCAAGTACCCGTTGGTGGCGGCCGCG | |
| Consensus | (541) | GCATTGTTGCACCC AAAATG ACTCTTATTGGGCCAAGTATCC GTGGTTCCGGCCGCG | |
| | | 601 | 660 |
| Fenugreek | (547) | ATGTTGGCCCATCCGCAAGTAGAATGCATATGCTGGTCCGACTCTGATCCCATCTTACG | |
| Guar-GalT1 | (589) | ATGATGGCCCATCCGGAAGTGGAGTGGCTGTGGTGGGTGGACTCGGACGCGTTTTCAG | |
| Guar-GalT2 | (562) | ATGATGGCCCATCCGGAAGCCGAGTGGATCTGGTGGGTCCGACTCGGACGCGTTGTTACG | |
| Consensus | (601) | ATGATGGCCCATCCGGAAGT GAGTGGAT TGGTGGGTCCGACTCGGACGCG T TTCACC | |
| | | 661 | 720 |
| Fenugreek | (607) | GATATGGAATTCAAGTTACCGTTATGGCGTTACAAGGATCACAACTTGTGATTTCATGGT | |
| Guar-GalT1 | (649) | GACATGGAGTTCAAGCTTCCGTTAAAGCGTTATAAGAACCAACATCTGTGGTTACCGGT | |
| Guar-GalT2 | (622) | GACATGGAGTTCAAACTACCAATTAGATTACTACAAGGATCACAACTCTGCTGTCATGGC | |
| Consensus | (661) | GACATGGAGTTCAAGCTACCGTTA AGCGTTACAAGGATCACAACT GTGGTTTCATGGT | |

FIGURE 7a (Sheet 1 of 3)

| | | | | |
|------------|--------|--|--|------|
| | | 721 | | 780 |
| Fenugreek | (667) | <u>TTGGGAAGAGTTGGTTAAGACAGAGCATAGTTGGACCGGGCTTAACGCGGGTGTTCCTTG</u> | | |
| Guar-GalT1 | (709) | <u>TTGGGAAGGATTGGTACGGTTGAACCATAGCTGGACCGGGCTTAACGCGGGCGTATTCTTG</u> | | |
| Guar-GalT2 | (682) | <u>TTGGGCCACCTCATCCACGAGAAACGTAGTTGGACCGGGCTCAACGCGGGCGTCTTCCTC</u> | | |
| Consensus | (721) | TTGGGAAGA TTGGT CAG GAA CATAGTTGGACGGG CT AACGCGGGCGT TTCTTG | | |
| | | 781 | | 840 |
| Fenugreek | (727) | <u>ATGAGGAATTGTCAATGGTCTGTGGATTATTATGGATGTTTGGGCCAGTATGGGCCCAAC</u> | | |
| Guar-GalT1 | (769) | <u>ATTTCGGAATTGCCAGTGGTCTGTGGACTTCATGGATGTTTGGGTGAGCATGGGCCACAG</u> | | |
| Guar-GalT2 | (742) | <u>ATCAGAAACGTGTCAATGGTCAATTGGACTTCATAAACGAATGGGCCAGCATGGGCCACAA</u> | | |
| Consensus | (781) | AT AGGAATTGTCAATGGTCTGTGGA TTCATGGATGT TGGGCCAGCATGGGCCACA | | |
| | | 841 | | 900 |
| Fenugreek | (787) | <u>AGCCCGGAATACGAGAAATGGGGGGAGAGACTTAGAGAAACTTTTAAACAAAGTGGTA</u> | | |
| Guar-GalT1 | (829) | <u>ACTCCGGAATACGAGAAATGGGGGGAGAGGTTCAGAGAGACATTCAAGGACAAAGTGGTG</u> | | |
| Guar-GalT2 | (802) | <u>ACTCCGAATACGAGAAATGGGGTCTAAACCTTAAGTCAACTTTCAAGACAAATCTTC</u> | | |
| Consensus | (841) | ACTCCGGAATACGAGAAATGGGGGGAGAG CT AGAGAAACTTTCAAGGACAAAGTG T | | |
| | | 901 | | 960 |
| Fenugreek | (847) | <u>CTGATTTCAGATGATCAGACGGCGCTGCTTACTTGATCGCGATGGGAGAG---GGACAAG</u> | | |
| Guar-GalT1 | (889) | <u>CCTGATTTCGACGATCAGACGGCGCTGCTTACCTGATCGCGACGGATAATAAGGACACG</u> | | |
| Guar-GalT2 | (862) | <u>CTCGGCTTCAGACGATCAGACGGCGCTGCTTACCTGATCGCGATCGAGAG---AGGAAAA</u> | | |
| Consensus | (901) | CCTGATTTCAGACGATCAGACGGCGCT GCTTACCTGATCGCGATGGA AA GGACAAG | | |
| | | 961 | | 1020 |
| Fenugreek | (904) | <u>TGGACAAAGAAGATCTATATGGAGAATGAGTATTATTTGAAGGGTATTTGGTTAGAGATT</u> | | |
| Guar-GalT1 | (949) | <u>TTGAGGGGAGAAGATCTTCTTGGAGCGGAGTACTACTTCGAAGGGTACTTGGTTCGAGATC</u> | | |
| Guar-GalT2 | (919) | <u>TTGGCCGGACAGATTTACTTAGAGAACTCGTATTATTTTGAAGGGTACTTGGGAGGAAATC</u> | | |
| Consensus | (961) | TGGACGGAGAAGATCTACTTGGAGAACGAGTATTATTTTGAAGGGTACTGG TAGAGATC | | |
| | | 1021 | | 1080 |
| Fenugreek | (964) | <u>TCAAAGATCTATGATAAATGGCTGAGAGATATGATGAGATAGAAAAGAGTGGGAAGGG</u> | | |
| Guar-GalT1 | (1009) | <u>GTGAAGACGTACGAGAACTAAGCGGAGGCTATGATGAGCTGGAGACGAGGTTGGAAGGG</u> | | |
| Guar-GalT2 | (979) | <u>GTCCGAACATTCGAGAAATAAGCAAGAAATACACAGAGATCGAAACGGGGGTGCGCAGG</u> | | |
| Consensus | (1021) | GT AAGACGTACGAGAA ATAAGCGGAGATATGATGAGAT GAAA GAGGGTGGGAAGGG | | |
| | | 1081 | | 1140 |
| Fenugreek | (1024) | <u>TTAAGGAGGAGGCATGCGAGAAAGTGAGTGAACTTATGCTGAAATGAGAGAGGAGTAT</u> | | |
| Guar-GalT1 | (1069) | <u>TTGAGGAGGAGGCATGCGGAAAGCTGAGCGAGAAATACGGTTCGATGAGGGAGGAGTAT</u> | | |
| Guar-GalT2 | (1039) | <u>TTAAGAAAGGCTTACGCGGAGAAAGTGAGTGAACTTACGGTGAGAGAGGGAAGATAT</u> | | |
| Consensus | (1081) | TTAAGGAGGAGGCATGCGGAGAAAGTGAGTGAA TTACGGTGAAATGAGGAGGAGTAT | | |
| | | 1141 | | 1200 |
| Fenugreek | (1084) | <u>GTTAAGAAATTTACGGGATAT-----CAGAAGACCTTTTATTACACATTTTACA</u> | | |
| Guar-GalT1 | (1129) | <u>CTGAAGGACA-----ACAA-----CAGGAGGCCCTTTATCAGCACTTTACT</u> | | |
| Guar-GalT2 | (1099) | <u>TTAAACCGAAGCGTAAACGGTAAAGGAAGCTGGAGACGGCCCTTGTGACGCACTTCAG</u> | | |
| Consensus | (1141) | T AAGGA AGG ACA GAGAAGGCC TTTAT ACGCACTTTAC | | |
| | | 1201 | | 1260 |
| Fenugreek | (1132) | <u>GGGTGCCAACCTTGTAATGGTCTATCATAATCQAATATATGCTGCAGATGATTGCTGGAAT</u> | | |
| Guar-GalT1 | (1171) | <u>GGGTGTCAACCTTGTAATGGCCACATAATCCTGCTTATAATGCTAATGATTGCTGGAAT</u> | | |
| Guar-GalT2 | (1159) | <u>GGGTGTCAACCTTGTAAGCGAATATATACCGCTATGTATAACGCCGAGATTGTTGGAAC</u> | | |
| Consensus | (1201) | GGGTGTCAACCTTGTAATGG CA CATAATCCTAT TATAATGC GATGATTGCTGGAAT | | |
| | | 1261 | | 1320 |
| Fenugreek | (1192) | <u>GGCATGGAGAGGCTCTCAATTGTCTGATAATCAGGTGTTGCGCAAGTTTGGTTTCATT</u> | | |
| Guar-GalT1 | (1231) | <u>GGCATGGAGAGGCTCTTAATTTTCGCTGATAATCAAACTTGGCTACTTACCGTTATCAC</u> | | |
| Guar-GalT2 | (1219) | <u>GGATGCGTAAGCCCTTAATTTTCGCTGATAATCAGGTGATGCGTAAATATGGTTTCGTA</u> | | |
| Consensus | (1261) | GGCATGGAGAGGCTCTTAATTTTCGCTGATAATCAGGTGTTGCGTAA TATGGTTTC T | | |
| | | 1321 | | 1380 |
| Fenugreek | (1252) | <u>CATCCAAATCTATTCGATAAGTCTGTTTCTCCATTACCAATTGGATA-CCCCGCTGCATC</u> | | |
| Guar-GalT1 | (1291) | <u>CGTCAAAATTTACTCGTCAAGTCTGTTTCACCTTACCTTTTGGTTA-CCGTGCTGCATA</u> | | |
| Guar-GalT2 | (1279) | <u>CACCCGGATGTACTAGATAATTCCTTTCGCGGATTCGGTTTGATTATCCCCGTAAACCGG</u> | | |
| Consensus | (1321) | CATCCAAAT TACT GATAAGTCTGTTTC CC TTACC TTTGGTTA CCCCCTGCATC | | |
| | | 1381 | | 1440 |
| Fenugreek | (1311) | <u>ACCATATAATA-TATTATAACCTGCAGGGGTG--AATTATAATAG-TAATTGTTATGATGA</u> | | |
| Guar-GalT1 | (1350) | <u>A-----TAATG-TACTACTAC-TG-----ATAACGACAG-TTATT-TAAAATTTA</u> | | |
| Guar-GalT2 | (1339) | <u>TCAGGTAATAATCATATTTAATTCGAATCTAATTATGTTGACCCCTGGCTACTCAGATTTC</u> | | |
| Consensus | (1381) | AC TAATA TA TATTAC TG A A AAT ATGACAG T ATT TTAAGATTA | | |
| | | 1441 | | 1500 |
| Fenugreek | (1367) | <u>TTCTTCTGTCAATAATAATCAAAATAATGAAGGTGGTGTGATATTAGC-----</u> | | |
| Guar-GalT1 | (1391) | <u>TTATAC-GAAAAAATAAATAAATAAAC-----</u> | | |
| Guar-GalT2 | (1399) | <u>TTCCATGCTGTCTGTAAAGTACTACTACTACTAGTATTAATTTCTAGTGATATTTTAT</u> | | |
| Consensus | (1441) | TTCTTCTGT AA AAAAATAAATAAAT GT T A T TTAG | | |

FIGURE 7b (Sheet 2 of 3)

| | | | | |
|------------|--------|---|------|------|
| | | 1501 | | 1560 |
| Fenugreek | (1416) | ----- | | |
| Guar-GalT1 | (1418) | ----- | | |
| Guar-GalT2 | (1459) | AATATTTTATTGTATATTTTCTGGCGTTTGCATATATAGTATCGTGTGGAGTAGTATT | | |
| Consensus | (1501) | | | |
| | | 1561 | | 1620 |
| Fenugreek | (1416) | ----- | | |
| Guar-GalT1 | (1418) | ----- | | |
| Guar-GalT2 | (1519) | TAATTATGCATAAGTGAAGGGATAATTTTATTCTTTTCGAATCCCTAAAAAAAAAAAAA | | |
| Consensus | (1561) | | | |
| | | 1621 | 1651 | |
| Fenugreek | (1416) | ----- | | |
| Guar-GalT1 | (1418) | ----- | | |
| Guar-GalT2 | (1579) | AAAAAAAAAAAAAAAAAAAAAAAAAACT | | |
| Consensus | (1621) | | | |

FIGURE 7c (Sheet 3 of 3)

| | | |
|----------------|---|-----|
| | 1 | 60 |
| Fenugreek-GalT | (1) ATKFG-SKN-KSSPWLSNGCIFLLGAMSALLMIWGLNSHIAPIPNPNPKFNSFTTKLKS | |
| Guar-GalT1 | (1) MAKFG-SRN-KSPKHTSNGCCFLGAFALLLLWGLCSFIPIPIHTDPKLNŠVATSLRSL | |
| Guar-GalT2 | (1) MAKSSNSRNKISHVNLSGCFLLGAFSAFLIVWGFSSFTTPIPNETPTPELSVNSHQ | |
| Consensus | (1) MAKFG SRN KS WLSNGCIFLLGAFSALLIIWGL SFI PIPNS PKFNSLST LKSL | |
| | 61 | 120 |
| Fenugreek-GalT | (59) NFTTN-TNFAGFDLLHDSKTFYDDPETCYTMMDKPMKNWDEKRKEWLFHHPSFAGAT | |
| Guar-GalT1 | (59) NFPKNPAATLPPNLOHDPDPTTFYDDPETSYSY-MDKPMKNWDEKRKEWLLHHPSGAAAR | |
| Guar-GalT2 | (61) DAVSR---GGDFRFDPPDRTFYDDPEMCGYT-IDTTVRDWDAREEWLRLHPSFAACAR | |
| Consensus | (61) NF SN AGPDL HDPDKTFYDDPET YT MDKPMKNWDEKRKEWL HHPFAAGAR | |
| | 121 | 180 |
| Fenugreek-GalT | (118) EKILVITGSQPTKCNPIGDHLLLRFYKNKVDYCRINHNDIYNNALLHPKMDSYWAKYP | |
| Guar-GalT1 | (118) DKILLVTGSQFKRCHNPIGDHLLLRFFKNKVDYCRILHNYDIIYNNALLHPKMNSYWAKYF | |
| Guar-GalT2 | (116) ERVLVVTGSQAPCRNPIGDHLLLRFFKNKVDYCRILHGYDIVYNNALLHPKMFYWAKYP | |
| Consensus | (121) EKILVVTGSQP KC NPIGDHLLLRFFKNKVDYCRILHNYDIIYNNALLHPKM SYWAKYP | |
| | 181 | 240 |
| Fenugreek-GalT | (178) MVRAAMLAHPEVEWIHWVSDAIFTDMEFKLPLWRYKDHNLVHGWEEVLKTEHSWTGLN | |
| Guar-GalT1 | (178) VIRAAMAHPEVEWVWVSDAVFTDMEFKLPLKRYKNHNLVHGWEGVLRLNHSWTGLN | |
| Guar-GalT2 | (176) VVRAAMAHPEAEWIHWVSDALFTDMFVKLPLDHYKDHNLVHGWHLTHEKRSWTGLN | |
| Consensus | (181) VVRAAMAHPEVEWIHWVSDAIFTDMEFKLPL RYKDHNLVHGWEE LK HSWTGLN | |
| | 241 | 300 |
| Fenugreek-GalT | (238) AGVFLMRNCQWSLDFMDVWASMGPNSEPEYKWERLRETFKTKVVRDSDDDQALAYLIAM | |
| Guar-GalT1 | (238) AGVFLIRNCQWSLEFMDVWVSMGPQTEPEYKWERLRETFKDKVLPSDDQALAYLIAT | |
| Guar-GalT2 | (236) AGVFLIRNCQWSLDFINENASMGBOTENYEKGQTLKSTFKDKFFPESDDQTGLAYLIAT | |
| Consensus | (241) AGVFLIRNCQWSLDFMDVWASMGPTPEYKWERLRETFKDKVLPSDDQALAYLIAT | |
| | 301 | 360 |
| Fenugreek-GalT | (298) G-EDKNTTKTYMENEFYFEGYWLEISKMYDKMGERLDEIEKRVEGLRRRHAEKVSEYGE | |
| Guar-GalT1 | (298) DNKDTNREKIFLSEYFEGYWLEIVKTYENISERNDEVERKVEGLRRRHAEKVSEKYGA | |
| Guar-GalT2 | (296) E-KEKNADKIYLENSYFEGYWLEIVGTENISKYNAETGVRRRLRRRHAEKVSEAYGE | |
| Consensus | (301) D KDKW DKTYLENEYYFEGYWLEIVKTYENISERYDEIEKKVEGLRRRHAEKVSEKYGE | |
| | 361 | 420 |
| Fenugreek-GalT | (357) MREEYVKNLG---DMRRPFIHTFTGCQPCNGHHNPIYAADDCWNGMERALNFADNQVLR | |
| Guar-GalT1 | (358) MREYMLKDNK-----RRPFIHTFTGCQPCNGHHNPAZNANDCWNGMERALNFADNQVLR | |
| Guar-GalT2 | (355) ERKYLTEAGNGKGSWRPFPVTHFTGCQPCSGKYNAMYNAEDCWNGMRKALNFADNQVLR | |
| Consensus | (361) MREEYKLD G RRPFIHTFTGCQPCNGHHNPIYNADDCWNGMERALNFADNQVLR | |
| | 421 | 451 |
| Fenugreek-GalT | (413) KGFTHPNLLDKSVSHLEFCYHAASP----- | |
| Guar-GalT1 | (412) TYGYHRONLLDKSVSHLEFCYPAA----- | |
| Guar-GalT2 | (415) KYGFVHPDVLNDSVSPIFEDYERNRSGNNHI | |
| Consensus | (421) KYGFTHPNLLDKSVSPLPFGYPAA | |

FIGURE 8

| | | |
|-----------|-------|--|
| | 1 | 60 |
| AtCesA1 | (1) | MEASAGLVAGSYRRNELVIRRHESDGG--TKPLKNMNGQICQICGDDVGLAETGDVFFVAC |
| ZmCesA1 | (1) | MAANKGMVAGSHNRNEFVMIRHDGDVPGSAKPTKSANGQVCQICGDSVGSATGDVFFVAC |
| GhCesA1 | (1) | -----MMESGVPVCHTCGEHVLNVNGEPFVAC |
| PtCesA | (1) | -----MMESGAPICHTCGEQVGH DANGELFVAC |
| CtManS | (1) | ----- |
| AtCslA9 | (1) | ----- |
| AtCslB1 | (1) | ----- |
| AtCslC4 | (1) | ----- |
| AtCslD1 | (1) | -----MASSPPKKTLSQSSSLRPPQAVKFGRR TSSGRIVSLSRDDMDVSGDYSQGN |
| AtCslE1 | (1) | ----- |
| AtCslG1 | (1) | ----- |
| Consensus | (1) | ----- |
| | 61 | 120 |
| AtCesA1 | (59) | NECAFPVCRPCY EYERKDG TQCCPQCKTRFRRHRGSPRVEGDEDEDVDDIENEFNYAQG |
| ZmCesA1 | (61) | NECAFPVCRPCY EYERKEGNQCCPQCKTRYKRQKGS PRVHGDEDEDVDDLNEFNKYQG |
| GhCesA1 | (29) | HECNFPICKSCFEYDLKEGRKACLR CGSPY-----D-ENLLDDVEK-ATGDQS |
| PtCesA | (29) | HECSYPMCKSCFEFEINEGRKVC LRCGSPY-----D-ENLLDDVEKKGSGNQS |
| CtManS | (1) | ----- |
| AtCslA9 | (1) | ----- |
| AtCslB1 | (1) | ----- |
| AtCslC4 | (1) | ----- |
| AtCslD1 | (55) | DYNYTVLMPPTPDNQAGSSGSTSES KGDANRGGG---GGDGPKMGNKLERRLSVMKS |
| AtCslE1 | (1) | ----- |
| AtCslG1 | (1) | ----- |
| Consensus | (61) | ----- |
| | 121 | 180 |
| AtCesA1 | (119) | ANKAR---HQRHGE EFSSSRHESQP-IPLLTHGHTVSGEIRT PDTQSVRTTSGPLGPSD |
| ZmCesA1 | (121) | SGKGPEWQLQGDDADLSSSARHEPHHRI PRLTSGQQISGEIPDASPDRHSIRS--P---- |
| GhCesA1 | (75) | TMAAHLN---KSQDVGIHARHIS-----S-----VSTLDSEMA----- |
| PtCesA | (76) | TMASHLN---DSQDVGIHARHIS-----S-----VSTVDSEMN----- |
| CtManS | (1) | ----- |
| AtCslA9 | (1) | ----- |
| AtCslB1 | (1) | ----- |
| AtCslC4 | (1) | ----- |
| AtCslD1 | (111) | NNKSMLLR SQTGDFDHNRLWFESK----- |
| AtCslE1 | (1) | ----- |
| AtCslG1 | (1) | ----- |
| Consensus | (121) | ----- |
| | 181 | 240 |
| AtCesA1 | (175) | RNAISSPYIDPRQVPVRI VDP SKDLNSYGLGNVDWKERVEGWKLKQEK NMLQMTGKYHE |
| ZmCesA1 | (175) | ----TSSYVDPSVPVPRIVDP SKDLNSYGLNSVDWKERVESWRVKQDKNM MQVTNKYPE |
| GhCesA1 | (105) | -----EDN-----GNSIWKNRVESWKEKKKNKKKKPATTKVER |
| PtCesA | (106) | -----DEY-----GNPIWKNRVKSKDKENKKKKRSPKAETE |
| CtManS | (1) | ----- |
| AtCslA9 | (1) | ----- |
| AtCslB1 | (1) | ----- |
| AtCslC4 | (1) | ----- |
| AtCslD1 | (135) | -----GKYGIGNAFWSEEDDTYDGGVSKS-- |
| AtCslE1 | (1) | ----- |
| AtCslG1 | (1) | ----- |
| Consensus | (181) | ----- |
| | 241 | 300 |
| AtCesA1 | (235) | GKGGEIEGTGSNGEELQMA DDTRLPM S RVVPIPSRLTPYRVVILRLIILCFFLQYRTT |
| ZmCesA1 | (231) | ARGGDMEGTGSNGEDMQMVDDARLPLSRIVPISSNQLNLYRVVILRLIILCFFFOYRV S |
| GhCesA1 | (137) | EAEIPPEQQ----MEDKPA PDASQPLSTIIPKSR LAPYRTVIMRLIILGLFFHYRVT |
| PtCesA | (138) | PAQVPTEQQ----MEEKPSA EASEPLSIVYPIPRNKLT PYRAVIMRLIILGLFFHFRVT |
| CtManS | (1) | ----- |
| AtCslA9 | (1) | ----- |
| AtCslB1 | (1) | ----- |
| AtCslC4 | (1) | -----MAPNSVAVTMEKPDNFSLLEINGSDPSSFPDKRKSISP KQFSWFLLLKAH |
| AtCslD1 | (159) | -----DFLDKPWKPLTRKVQIPAKILSPYRLLIIVIRLVIVFFFLWRRIT |
| AtCslE1 | (1) | -----MVNKDDRIRPVHEADGEPLFETRRTGRVIA YRFFSASVFVCICLIWFYRIG |
| AtCslG1 | (1) | -----METHRKNSVVGNI LHTCHPCRRTIPYRIYAFHTCGI IALMYHHVH |
| Consensus | (241) | D S L YR II I L F YRI |

FIGURE 9a (Sheet 1 of 4)

| | | | |
|-----------|-------|--|-----|
| | 301 | | 360 |
| AtCesA1 | (295) | HPVKN---AYPLWLTSVCEIWFASFSLDQFPKWYPINRETYLDRLAIRYDRDGEP-- | |
| ZmCesA1 | (291) | HPVDR---AYGLWLVSVICEVWFALSLLDQFPKWYPINRETYLDRLAIRYDRDGEP-- | |
| GhCesA1 | (193) | NPVDS---AFGLWLTSVCEIWFASFSLDQFPKWYPVNRRETYIDRLSARYEREGERP-- | |
| PtCesA | (194) | NPVDS---AFGLWLTSVCEIWFASFSLDQFPKWVNRRETYIERLSARYEREGERP-- | |
| CtManS | (1) | ----- | |
| AtCslA9 | (1) | ----- | |
| AtCslB1 | (1) | --MNQ---NNSVWVVAFLCESEFSFIWLLITSIKNSPASYKSYPERLDERVH----- | |
| AtCslC4 | (51) | RLISC---LSWLVS SVKKRIAFSAKNINEEEDPKSRGKQMYRFKACLVISIIALSI-- | |
| AtCslD1 | (203) | NPNE---AMWLWGLSVCEIWFASFSLDILPKLNPNRATDLAALHDKFEQSPSPNP | |
| AtCslE1 | (53) | EIGDNRTVLDRLWFMFVEIWFGLYVVTQSSRWNPVWRFPFSDRLSRRYG----- | |
| AtCslG1 | (47) | SLVTAN---NTLITCLLLSDIVLAFMWATTTSLRLNPFVHRTECPKYAAKPE----- | |
| Consensus | (301) | V LW SVCEIWF AF WLLD PKW PVNR TYIDRLA RYE | |
| | 361 | | 420 |
| AtCesA1 | (349) | ---SQLVPDYFVSTVDPDKKEPPLVTANTVLSLSVDYVPDKVACYVSDDGSAMLTFFESL | |
| ZmCesA1 | (345) | ---SQLAPIDYFVSTVDPDKKEPPLVTANTVLSLSVDYVPDKVACYVSDDGSAMLTFFESL | |
| GhCesA1 | (247) | ---DELAADVDFVSTVDPDKKEPPLVTANTVLSLALDYVPDKVACYISDDGAAMLTFFESL | |
| PtCesA | (248) | ---SQLAGVDFVSTVDPDKKEPPLVTANTVLSLAVDYVPDKVACYVSDDGAAMLTFFESL | |
| CtManS | (1) | -----MRNLIFEPEGIPGNSSSLRYAWQSIRAPVILPLKLAIVICSVMSIM | |
| AtCslA9 | (1) | -----MEIGDTTSVIPDSFMGYRDDITMQSMVLDQIRAPLIVPALRLGVYICLTMSVM | |
| AtCslB1 | (48) | ---DLPSVDMFVTADDPREPPILVANTVLSLAVNYPANKLACYVSDDGCPLTVFSL | |
| AtCslC4 | (105) | ---EIVAHFKKWNLDINRPSWEVYGLVIEWSYMAWLSERSDYIAPLVISLSRFTVLFIL | |
| AtCslD1 | (259) | TGRSDLPGVDFVSTADPEKEPPLVTANTVLSLAVDYPIEKL SAYTSDDGAILTFEAM | |
| AtCslE1 | (106) | ---SDLPRLDVFCCTADDPVIEPPLVVNTVLSVTALDYPPKLA VYLSDDGGSELTFFAL | |
| AtCslG1 | (97) | ---DFPKLDVFCCTADDPYKEPPMMVNTALSVMAYEYPSDKISVYVSDDGGSELTFFAL | |
| Consensus | (361) | L VDFVSTVDPDKKEPPLI ANTVLSILAVDYP DKIS YVSDDG A LTF SL | |
| | 421 | | 480 |
| AtCesA1 | (406) | SETAEFAKKWVPFCKKFNIEPRAPPEFYFAOKIDYLDKDKIQ--PSFVKERRAMKREYEEFK | |
| ZmCesA1 | (402) | SETAEFAKKWVPFCKKFNIEPRAPPEFYFAOKIDYLDKDKIQ--PSFVKERRAMKREYEEFK | |
| GhCesA1 | (304) | VETADFARKWVPFCKKFSIEPRAPPEFYFSOKIDYLDKDKVQ--PSFVKERRAMKRDYEEFK | |
| PtCesA | (305) | VETAEFAKKWVPFCKKFSIEPRAPPEFYFSOKIDYLDKDKVQ--PSFVKERRAMKRDYEEFK | |
| CtManS | (50) | LFVERVMAAAILIVKVLKKRYTKYNLEAMKQKLSK--YPMVLIQIPMYKEVYK | |
| AtCslA9 | (55) | LFVERVYMGIVISLVLFGRKPKDKREKYEPIKDDIELGNSA-YPMVLIQIPMFNEREVYQ | |
| AtCslB1 | (104) | KEASKFAKIWVPFCKKYNIKVRAPFRYFLNPPAATSS----EFSKDWEITKREYKLS | |
| AtCslC4 | (162) | QSLDLVLCLGCFWIKKK---IEPKLTEESIDLEDPS--FPMVLIQIPMCNEREVYE | |
| AtCslD1 | (319) | AEAVRFAEYWVPFCKKHDI EPRNPDSYFSIKKDPKTKNKR--QDFVKDRRWIKREYDEEK | |
| AtCslE1 | (163) | TEAAEFAKTWVPFCKKFNVEPTSPAAYLSKANCDSAAE--EVAKLYREMAAR--IETA | |
| AtCslG1 | (153) | IEAAKFSKQWLPFCKKNNVQDRSPEVYFSSESHRSDEAENLKTNTLKCEVEQMMYEDMK | |
| Consensus | (421) | E ARFAK WVPFCKKF IEPRAPPEFYFS K D L D FVKER MKREYEEYK | |
| | 481 | | 540 |
| AtCesA1 | (464) | VRINALVAKAOKIPEEG-----WTMQDGTWPWPGNN | |
| ZmCesA1 | (460) | VRINALVAKAOKVPEEG-----WTMADGTAWPGNN | |
| GhCesA1 | (362) | VRINALVAKAOKTPDEG-----WTMQDGTWPWPGNN | |
| PtCesA | (363) | VRINALVAKAOKTPDEG-----WTMQDGTWPWPGNN | |
| CtManS | (108) | LSIGAVCGLSWPADRFI-----VQVLDDSTNP-- | |
| AtCslA9 | (114) | LSIGAACGLSWPSDRIV-----IQVLDDSTDP-- | |
| AtCslB1 | (159) | RRVEDATGDSHWLDAED-----DFEDFSNTK | |
| AtCslC4 | (216) | QSIGAASQLDWPKDRIL-----IQVLDDSDDP-- | |
| AtCslD1 | (377) | VRINGLPEQIKKRAEQFNMREELKEKRIAREKNGGVLPPDGVEVVKATWMADGTHWPGTW | |
| AtCslE1 | (219) | ARLGRIPPEARVKYGDG-----FSQWDADA | |
| AtCslG1 | (213) | SRVEHVVESGKVETAFIT-----CDQFRGVFDLWTDKF | |
| Consensus | (481) | VRI AL A A E M D T WPG | |
| | 541 | | 600 |
| AtCesA1 | (494) | TR-----DHPGMIQ-VFLGHSGGLDTDGNE-----LPRLIVVSREKRPGE | |
| ZmCesA1 | (490) | PR-----DHPGMIQ-VFLGHSGGLDTDGNE-----LPRLIVVSREKRPGE | |
| GhCesA1 | (392) | PR-----DHPGMIQ-VFLGYSGARDIEGNE-----LPRLIVVSREKRPGE | |
| PtCesA | (393) | TR-----DHPGHDSGLPWEILGARDIEGNE-----LPRLIVVSREKRPGE | |
| CtManS | (135) | -----VIRELVEMECQKWIQK-----V-NVKYENRNRNGY | |
| AtCslA9 | (141) | -----TIKDLVEMECRSWASKG-----VNKYEIRDNNGY | |
| AtCslB1 | (185) | PN-----DHSTIVK-VVWENKGGVGVEN-----EVPHFVYISREKRPNY | |
| AtCslC4 | (243) | -----NLQLLIKEEVSVAEKG-----V-NIYRHRLIRTGY | |
| AtCslD1 | (437) | FEPKPDHSGDHAETLQIMSKVPDLEPVMGPGNEGALDFTGIDIRVPMFAVVSREKRPGE | |
| AtCslE1 | (244) | TRR-----NHGTILQVLVDGREG-----N-TIAIPTLYLSREKRPQH | |
| AtCslG1 | (246) | SR-----HDHPTILQVLQNSD-----KYIMPNIIVVSREKSKVS | |
| Consensus | (541) | R DH IIQ L G DG LP LVVVSREKRPGE | |

FIGURE 9b (Sheet 2 of 4)

| | | | |
|-----------|-------|--|-------------|
| | 601 | | 660 |
| AtCesA1 | (533) | QHHKAGAMNALIRVSAVL T NGAYLLNV C DHYFNNSKAIKEAMCFMMDPA-IGKKCCYV | |
| ZmCesA1 | (529) | QHHKAGAMNALIRVSAVL T NGAYLLNV C DHYFNSSKALREAMCFMMDPA-LGRKTCYV | |
| GhCesA1 | (431) | QHHKAGAENALVRVSAVL T NPFLN L DCDHYVNNKAVREAMCFMMDPQ-VGRDVCYV | |
| PtCesA | (433) | QHHKAGAENALVRVSAVL T NPFLN L DCDHYVNNKAVREAMCILMDPQ-VGRDVCYV | |
| CtManS | (166) | KAGALKEGLEKQY-----VEDCEPVAIFDAD F QPDADFLWNTIPYLLLENPK-LGLVQARW | |
| AtCslA9 | (172) | KAGALKEGMKKS-----VKSCDYVAIFDAD F QPEADFLWRTVPYLLHNPK-LALVQARW | |
| AtCslB1 | (223) | LHHYKAGAMNFLVRVSG L MTNAPYMLN V DCMYANEADVVRQAMCIFIQKSMNSNHCAEV | |
| AtCslC4 | (274) | KAGNLKSAMTCDY-----VKDYEFVTIFDAD F TNPDPFLKKTVPHEKGNPE-LGLVQARW | |
| AtCslD1 | (497) | DHNKKAGAMNGMVRASAIL S NGAFILN L DCDHYIYNSKAIKEGMCFFMDR--GGDRI C YV | |
| AtCslE1 | (281) | HHNFKAGAMNALIRVSSKITCGKITLNL L CDMYANNSKSTRDA T CIL L DEK-EGKEIAEV | |
| AtCslG1 | (287) | PHHFKAGALNTLIRVSGVMTNSPI L TLTLC D MYSNDPATLVRA L CYLTDP-EIKSGLGYV | |
| Consensus | (601) | HH KAGAMNALVRVSAVL T NG YILN L DCD Y N SKAVREAMCFLM D P LG AYV | |
| | 661 | | 720 |
| AtCesA1 | (592) | QFPQRF D GIDLH D RYANRNIVFFDIN M KGLDGIQGPVYVGTGCCFN R QALYGYDPVLTEE | |
| ZmCesA1 | (588) | QFPQRF D GIDLH D RYANRNIVFFDIN M KGLDGIQGPVYVGTGCCFN R QALYGYDPVLTEA | |
| GhCesA1 | (490) | QFPQRF D GIDRS D RYANRNIVFFDIN M KGLDGIQGPVYVGTGCVFN R QALYGYGPPSMPS | |
| PtCesA | (492) | QFPQRF D GIDKSDRYANRNIVFFDIN M KGLDGIQGPVYVGTGCVFN R QALYGYGPPSMPS | |
| CtManS | (220) | KVINSEECMT R LQEMSLDYHFSVEQEVGSSTYSFFG N GTAGVWRIQATK D AG----- | |
| AtCslA9 | (226) | KVINSEECMT R QEMSLDYHFTVEQEVGSSTYAFFG N GTAGIWRISALNEAG----- | |
| AtCslB1 | (283) | QFPQEF---Y--DSNADELTVLQSYLGRGTAGI Q GPTYAGSGCFHTRRVMYGLS----- | |
| AtCslC4 | (328) | SPV N KDENL L TRLQNINLCFHFVEQOVNGVFLNFFG N GTAGVWRIKALEESG----- | |
| AtCslD1 | (555) | QFPQRFEGIDPS D RYANHNTVFFDGNMRALDGIQGPVYVGTGCMFRRYALYGFNPP---R | |
| AtCslE1 | (340) | QFPQCFD N VTRNDLYGSMRVDI V EFLGLDGGGPLYIGTGC F HRRDVICGRKYG---- | |
| AtCslG1 | (346) | QFPQKFLGISKN D IYACENKRLFI N VMVGFDGLMGPTHVGTGC F FNRRAFYGP----- | |
| Consensus | (661) | QFPQRF D GI D YAN N VFFDIN M KGLDGIQGPVYVGTGCVF R ALY | |
| | 721 | | 780 |
| AtCesA1 | (652) | DLEP---NII V KSCCGSRKKGKSSKKYNYEKRRGINRSDSNAPLFN M EIDEGFEGYDDE | |
| ZmCesA1 | (648) | DLEP---NIVIKSCCGRRK--KNKSYMDSQSRIMKRTESSAPIFN M EIEEGIEGYEDE | |
| GhCesA1 | (550) | FPK--SSSSSCSCCPGKKE---PKDPSELYRDAKRELDAAIFN L REIDN---YDEYE | |
| PtCesA | (552) | LRRKRDSSSCFSCCPSKKKP---AQDPAEVYRDAKREDLNAAIFN L TEIDN---YDEHE | |
| CtManS | (274) | ----- | |
| AtCslA9 | (280) | ----- | |
| AtCslB1 | (332) | -----ID D LEDGSLSSLA | |
| AtCslC4 | (382) | ----- | |
| AtCslD1 | (612) | -----ANEYSGVFGQEKAPAMHVRTQSQASQTSQASDLES T QPLN D DPDLGLPKKFG | |
| AtCslE1 | (396) | ----- | |
| AtCslG1 | (400) | -----Y M | |
| Consensus | (721) | | L D |
| | 781 | | 840 |
| AtCesA1 | (709) | RSILMSQRSVEK R EGQSPVFIATFMEQGG----IPPTNPATL L KEAIHVISC G YE D K | |
| ZmCesA1 | (703) | RSVLMSQRKLEK R EGQSPIFIATFMTQGG----IPPSTNPASL L KEAIHVISC G YE D K | |
| GhCesA1 | (601) | RSMLISQTSFEK T EGLSSVFIESTLMENG--VAESANPSTL L KEAIHVISC G YE E K | |
| PtCesA | (606) | RSMLISQLSFEK T EGLSSVFIESTLMENG--VPESANSPPF L KEAIQVIG C GYE E K | |
| CtManS | (274) | -----G----- | |
| AtCslA9 | (280) | ----- | |
| AtCslB1 | (346) | TRKYLAENLAR E FGNSNEMVTSVVEALQRK---PNPQNTLAN S IEAAQEVGHCH E YQ | |
| AtCslC4 | (382) | -----G----- | |
| AtCslD1 | (665) | NSTMFTD T IPVAEYQGRPLADHMSVKNGRPPGALLLPRP L DAPTVAEAI A VISCWYE D N | |
| AtCslE1 | (396) | -----EEEEEE-----SERIHENLEPEMIKALASCTYE E N | |
| AtCslG1 | (402) | LILPEIN--ELK P YR-----IADKSIKAQDV L SLAHNVAGCIYE Y N | |
| Consensus | (781) | K F | L A V C YED |
| | 841 | | 900 |
| AtCesA1 | (764) | TEWGKEIGW T YGSV T EDILTGF K MHARG S ISTYCNPP R PAFKGSAPINLS D RLN Q VL R NA | |
| ZmCesA1 | (758) | TEWGKEIGW T YGSV T EDILTGF K MHARG S QSTYCMPP R PCFKGSAPINLS D RLN Q VL R NA | |
| GhCesA1 | (656) | TAWGKEIGW T YGSV T EDILTGF K MHCRG S WRSTYCMPL R PAFKGSAPINLS D RLH Q VL R NA | |
| PtCesA | (661) | TEWGKQIGW T YGSV T EDILSC F KMHCRG S WRSTYCMPV R PAFKGSAPINLS D RLH Q VL R NA | |
| CtManS | (275) | -----WKDRITVEDMDLAVRASLHGWEFVEVG--DVKVKNELSTFKAYR F QHRWS | |
| AtCslA9 | (280) | -----GWKDRITVEDMDLAVRASLKGWKF L YLG--SLKVKNELSTFKAYR V QHRWS | |
| AtCslB1 | (402) | TSWGTIGW L YESTAE D ANTSIG I HSRGWTS S YISPKPPAFLGAMP P GGPEAM L QRR N A | |
| AtCslC4 | (383) | -----WLERITVEDMDIAVRAHLNGWK F TYLN--DVEVTCEL P ESYEAYKK Q HR N H | |
| AtCslD1 | (725) | TEWGDRIGW T YGSV T EDVVTGYRMHNRG S WRSTYCYITK R DAF R GTAPINLT D RLH Q VL R NA | |
| AtCslE1 | (427) | TQWGKEMGVKYGCPVEDVITGLTIQCRG S KAYLNPEKQAF L GVAPTNLH Q MLV Q ORR N S | |
| AtCslG1 | (441) | TNWGSKIGFRYGS L VEDYITGFM L HCEG S WRSTYFCNP K KAAFYGD S PKCLVD L V Q QIR N A | |
| Consensus | (841) | T WGK IGWIYGSV EDILTGF K MH RGWRSIY C P R AFKG AP NL D L QQLRWA | |

FIGURE 9c (Sheet 3 of 4)

901 960

AtCesA1 (824) LGSVEILLSRHCPIWYGYHG-RLRLERLAYINTIVYPITSIPLIAYCILPAFCLITDRF
ZmCesA1 (818) LGSVEILLSRHCPIWYGYNG-RLKLLERLAYINTIVYPITSIPLIAYCVLPALCLLTNKF
GhCesA1 (716) LGSVEIFFLSRHCPWYGFGGRLKWLQRLAYINTIVYPITSIPLIAYCSLPAICLLTGKF
PtCesA (721) LGSVEIFFSRHCPLWYGFGGRLKWLQRLAYINTIVYPITSIPLIAYCTIPAVCLLTGKF
CtManS (325) CGPANLFRKMTKEICCKR----VPLLKRLHLIYAFFVRKIYAHWVTFPPYCIVIPAC
AtCslA9 (331) CGPANLFRKMAFEIMTNKN----VTLWKKVHVIYSFFVVRKLVAHIVTFIFYCVLPAT
AtCslB1 (462) TGLLEVLFNKQSPITGMFCR-KIRFRQSLAYLYIFTWGLRSIPETIYCLLPAYCLLHNAA
AtCslC4 (433) SQPMQLFRCLCLPSIIKSK----TSVWKKANLIFLFLLRKLIIPFYSFTLFCITLPLT
AtCslD1 (785) TGSVEIFFSKNNNAMEATR--RLKFLQRAYINVGIYPPTSIPLIYVYCFPLPALCLFSGKF
AtCslE1 (487) EGDQIMLSKYSPVWYKGG-KTSLGLILGYCCYCLWAPSSLPVLIYSVLTSLCLFKGIP
AtCslG1 (501) VGLPEMSPSKYSPITYGIKS--LDLLMGLGYCNSPFPKFWSTPLTVYGLLPQALISGVS
Consensus (901) G VEIF SKH PIWYG RLKLL LAYIN VYP TSIPLI YC LPALCLIT

961 1020

AtCesA1 (883) IIPETSNYASIWFLILFISIAVTGILELRWSGVSTEDWRNEQFWVIGGTSAHFLAVFQG
ZmCesA1 (877) IIPETSNYAGMFFILLFASIFATGILELRWSGVSTEDWRNEQFWVIGGTSAHFLAVFQG
GhCesA1 (776) IIPETSNLASVLFGLFLSIIVTAVLELRWSGVSTEDLWRNEQFWVIGGVS AHFLAVFQG
PtCesA (781) IIPETSNLASMLFLGLFISIIVTAVLELRWSGVSTEDLWRNEQFWVIGGVS AHFLAVFQG
CtManS (380) IIVPEVNLKKQIATYTPATITILNAVSTPRSMHLIVLWILFENVMSLHRTKAAITGLLE-
AtCslA9 (386) IIVPEVTVPKGAIVYIPSVITILNAVGTPRSLHLMVFWILFENVMSLHRTKATFGLLE-
AtCslB1 (521) LFP--KGVYLGIVTLVGMHCLYSIWEFMSLGFVSQSWFASQSFWRIKTTCQWLFSTPDI
AtCslC4 (487) MFIPEAEPLWITICYVPIFISLNLPLSPKSFPPFVPLLFENTMSITKFNAMISGLFQ-
AtCslD1 (842) IVQSIDIHFLSYLCTITVTLTILISLEVKNWSGIGLEEWWRNEQFWVIGGTSAHFLAAVQVQ
AtCslE1 (545) IIPKVSSSWFIPFGYMTVAATAYSLAEFLWCGGTFRGWNEQRMWLYRRTSSFLFGMDT
AtCslG1 (559) VFPKASDPFWLYLILFFGAYAQDLSDFLLEGGTYRKWWDQRMIMIKGLSFFFGFIEF
Consensus (961) IIP LS L IFI L ISI L LLE WSG SI WW EQFWVI GTSA LFAV Q

1021 1080

AtCesA1 (943) ILKVLGIDTNFTVFSKATDE--DGDFEAL-----MFKWTALLIPPTTVI
ZmCesA1 (937) ILKVLGIDTNFTVFSKASDE--DGDFEAL-----MFKWTSLLIPPTTVI
GhCesA1 (836) FLKMLGIDTNFTVFAKAA-D-DADEGEL-----MVKWTLLIPPTTVI
PtCesA (841) FLKMLGIDTNFTVFAKAA-E-DADEGEL-----MVKWTLLIPPTTVI
CtManS (439) ---AN-RVNEWVTEKLG-----NA-----MKQRNARPS---
AtCslA9 (445) ---GGRVNEWVTEKLG-----DVKAKSATKT-
AtCslB1 (579) ILKVLGISKTVFIVTKTMPKTMMSGSGSEKSQREVDCPNQDSGKEFDGSLYFPGTFTI
AtCslC4 (546) ---FG-SAYEWVVEKGTG-----RS-----SESDLLAFAEKEEK
AtCslD1 (902) ILKVIAGIEISFTLTSKASGEDEDDIADL-----MVKWTGLFIMPLTII
AtCslE1 (605) ILKVLGVSESAFVITAKVABEEAAERYKEEVMEFG-----VESPMFVLGTIG
AtCslG1 (619) ILKTLNLSTPKFNVTSKANDDDEQRKRYEQEIFDFG-----TSSSMFPLTTVA
Consensus (1021) ILKVLG DT F VTSKAA E F E Y K T L IP TTLL

1081 1140

AtCesA1 (987) LVNLIGIVAGVSYAVNSGYQSWGPLFGKIFFALVTAHLYPFLKGLLGRQNR-----
ZmCesA1 (981) LVNLVGMVAGISYATNSGYQSWGPLFGKIFFSIWVTHLYPFLKGLMGRQNR-----
GhCesA1 (879) LVNMGVAGVSDALNKGYEAWGPLFGKIFFSFWVTHLYPFLKGLMGRQNR-----
PtCesA (884) LVNMSG-CAGFSDALNKGYEAWGPLFGKIFFAFWVTHLYPFLKGLMGRQNL-----
CtManS (465) -----RASRFRIIERIH-----
AtCslA9 (469) -----S-----K---KVIRFRFGDRIHV-----
AtCslB1 (639) LVN-LAALAGCSVGLQRHRGG-GSGLAEACGCILVVILFLPFLKGMFEKKG-----
AtCslC4 (576) LHRNS--ESGLELTKLKEQETNLVGQETVKKSLGGLMRPKNKKTNMVF-----
AtCslD1 (948) LVNLVAIVIGASRTIYSVIPQWGLMGGIFFSLVITHMYPPFAKGLMGRRGK-----
AtCslE1 (653) MLNDFCFAAAVARLVSGDGDLDKTMGMQFVITGVLVVINWPLYKGLLRQDK-----G
AtCslG1 (668) LVNLLAFVWGLYGILFCG----GELYELMLVSEAVVNCLPIYGMVLRKDDGLSKRTC
Consensus (1081) IVNLVG VAG S L G L G L WVIL LYPF KGLM R

1141 1192

AtCesA1 (1039) -TPTIVVWSVLLASIESLWVRINPFVDANPNANNFNGKGGVF-----
ZmCesA1 (1033) -TPTIVVWSVLLASIESLWVKIDPFTSPTQKAALGQCGVNC-----
GhCesA1 (931) -TPTIVVWSVLLASVFSLVWVRINPFVSTADSTTVSQSCISIDC-----
PtCesA (935) -TPTIVVWSVLLASVFSLVWVKINPFVKNVDNLVAETCISIDC-----
CtManS (477) -PLEIVGMYMLHCATYDLEFGHDHFFVYLLLOAGAFFTMGFLVGTIVPT-
AtCslA9 (484) --LELVGVMYLFLVGCYDAFEGKNHYLYLFAQAIAFFIAGFGQIGTIVPNH
AtCslB1 (688) ----YGIPTSLSKAEFLAVLVVFSVGN-----
AtCslC4 (625) -KKEIGLAFLLLTAAARSFLSAHGLHFYLLFQGLSFLVVGDLDIGEQIS--
AtCslD1 (1000) -VPTIVVWSGLVSTVSLWITISPPDDVSGSGGISV-----
AtCslE1 (706) KPMPSVTVKSIVLALSACTCLAFI-----
AtCslG1 (724) FLAGNLHVGSYCVKLLRPQVTSPLRIHNNTSGWFKRKKHNMNESV-----
Consensus (1141) P IVVVWSVLLAS FSLW I FV A

FIGURE 9d (Sheet 4 of 4)

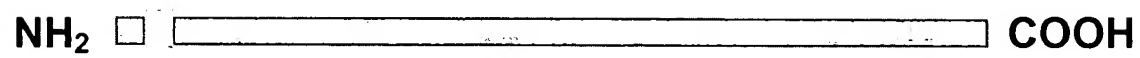
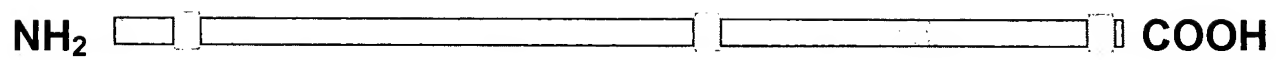


FIGURE 10

R S L 10 25 30 E SC Em

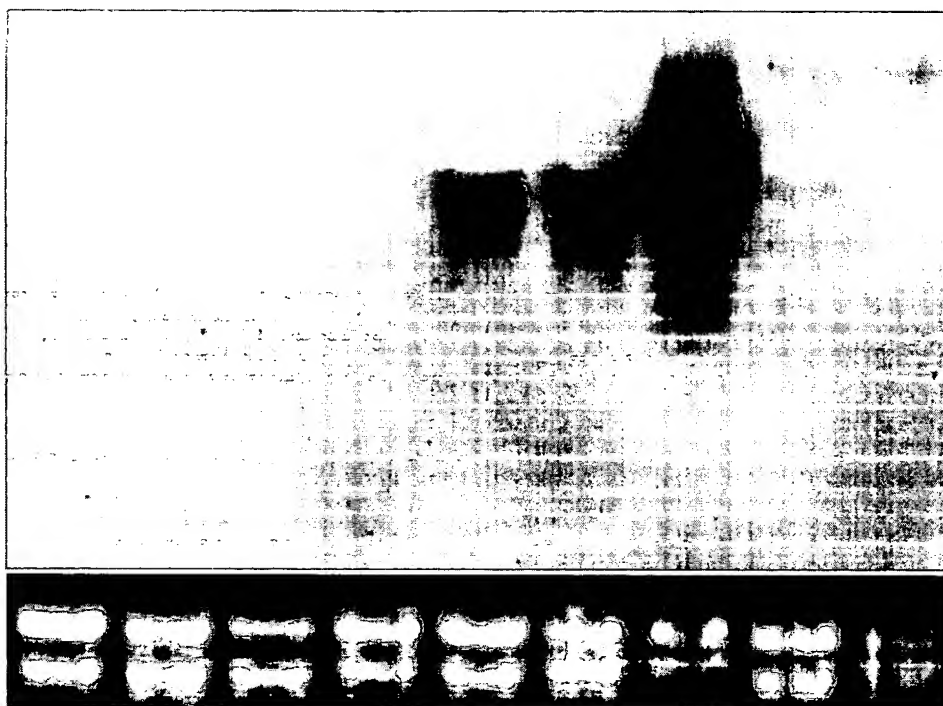


FIGURE 11

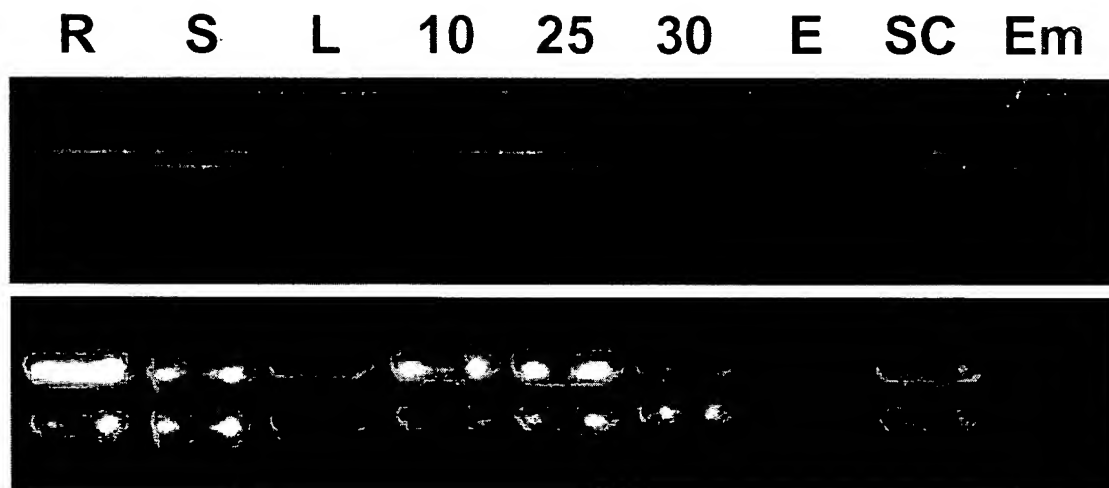


FIGURE 12A

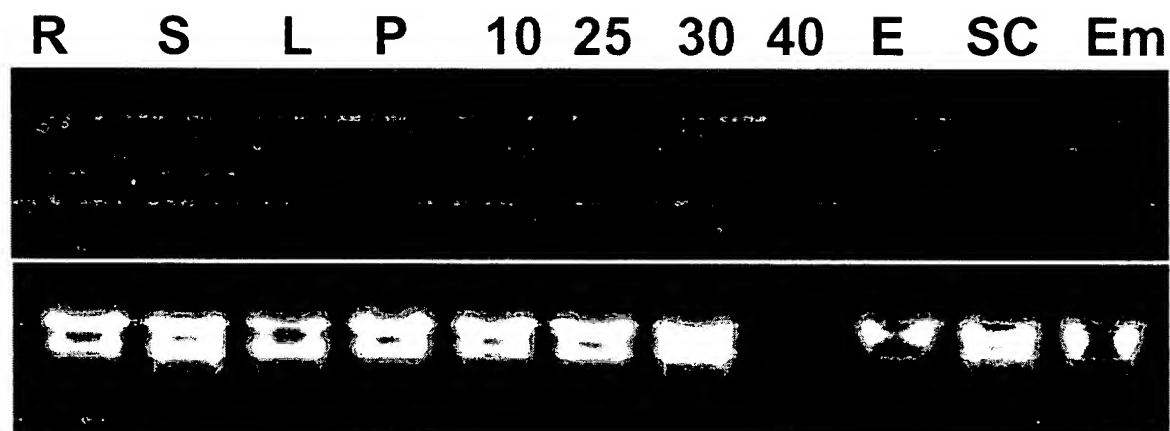


FIGURE 12B

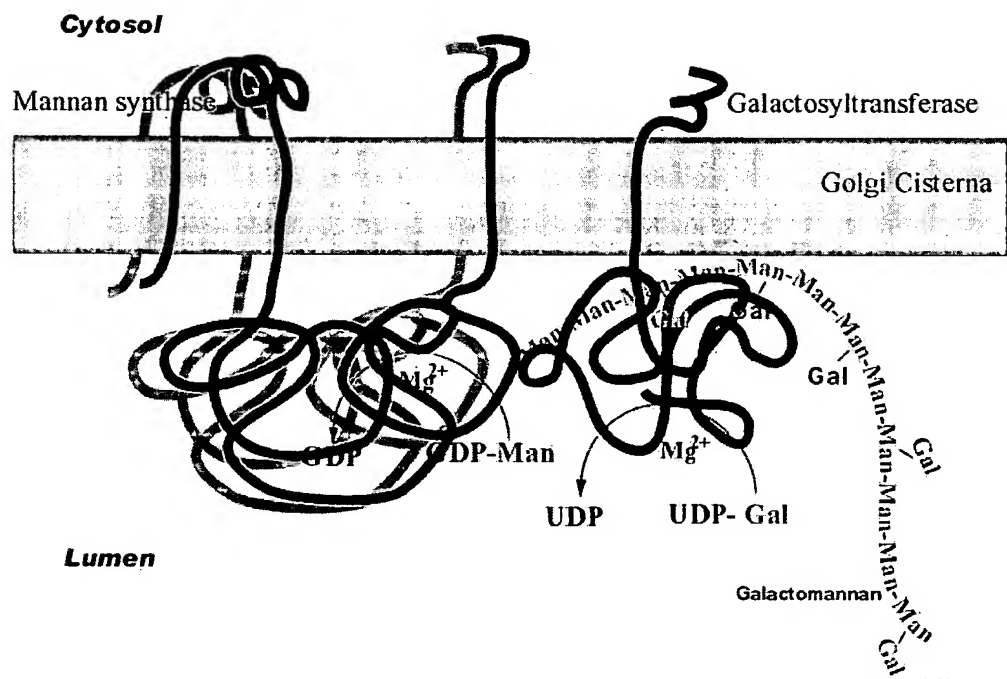


FIGURE 13

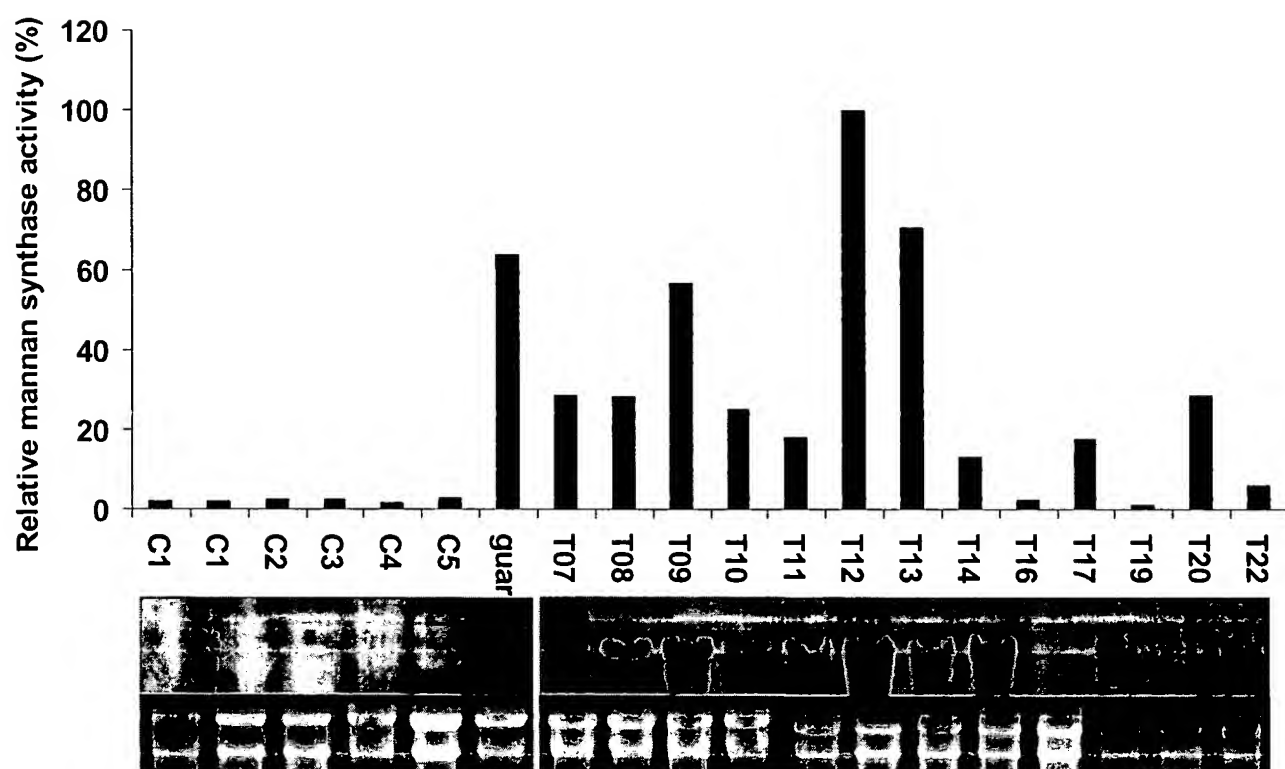


FIGURE 14

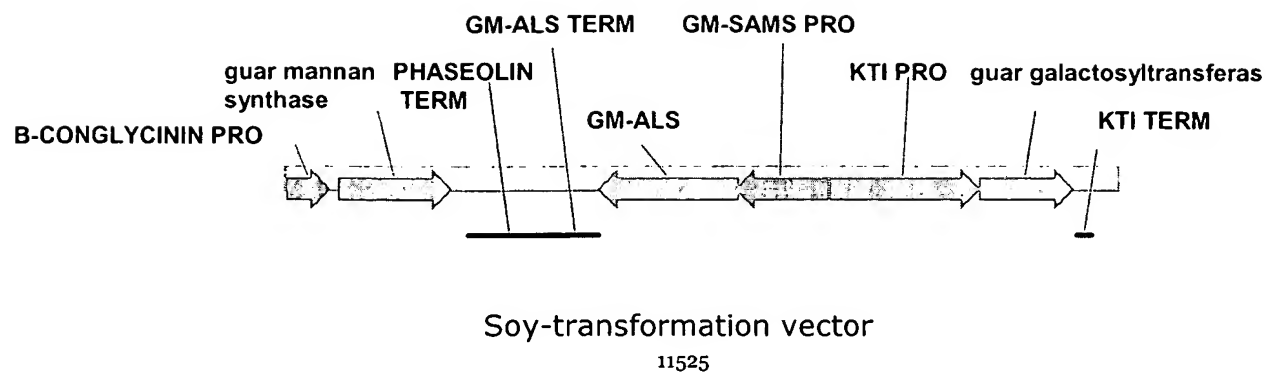


FIGURE 15

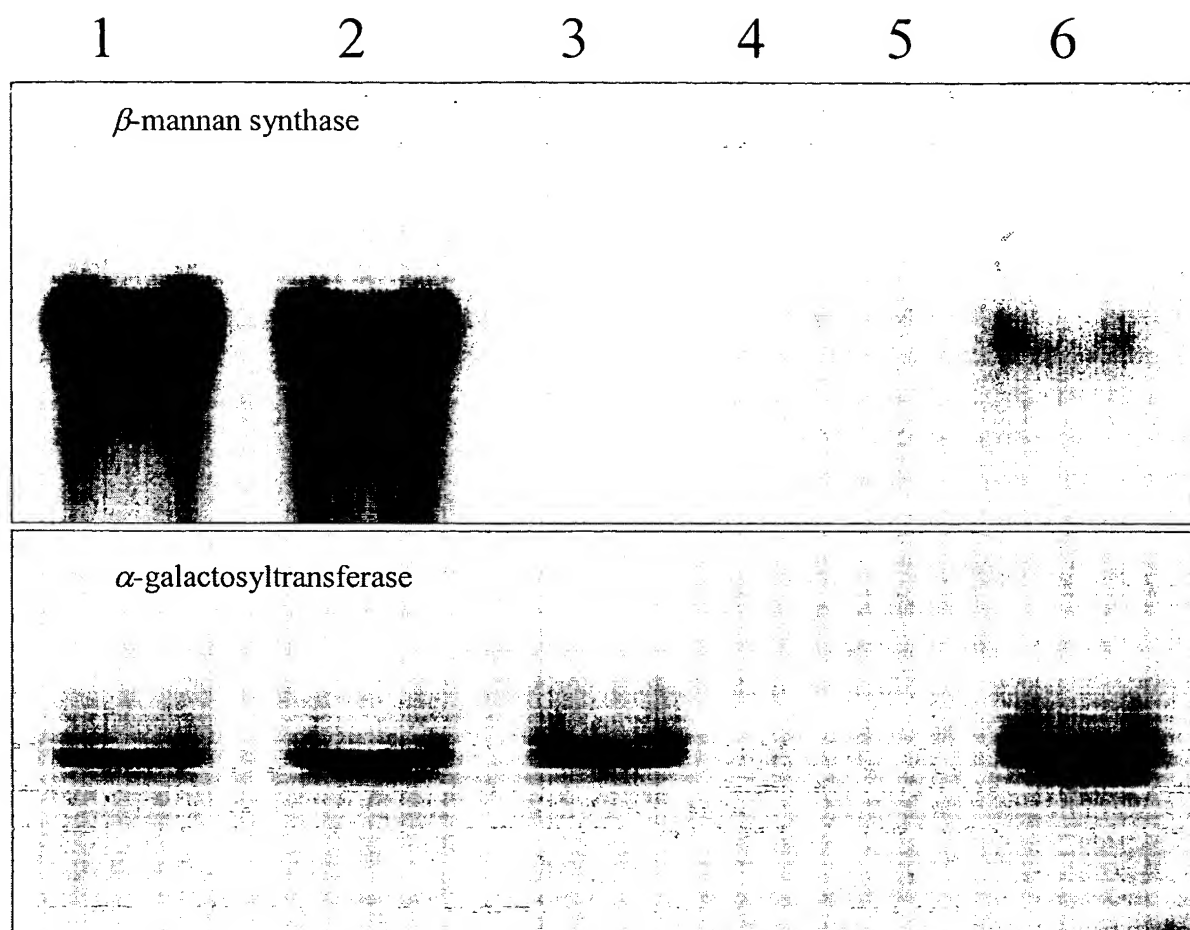


FIGURE 16

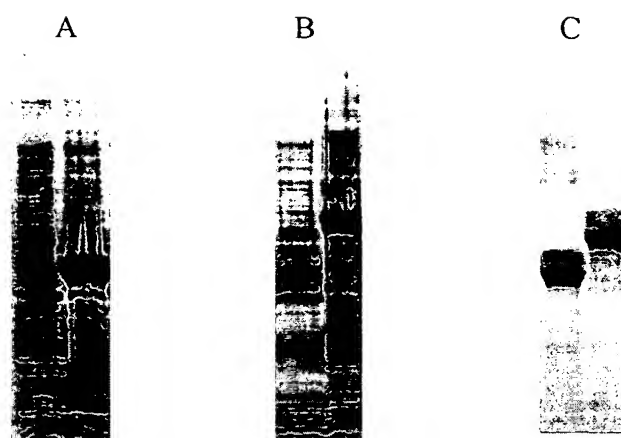


FIGURE 17

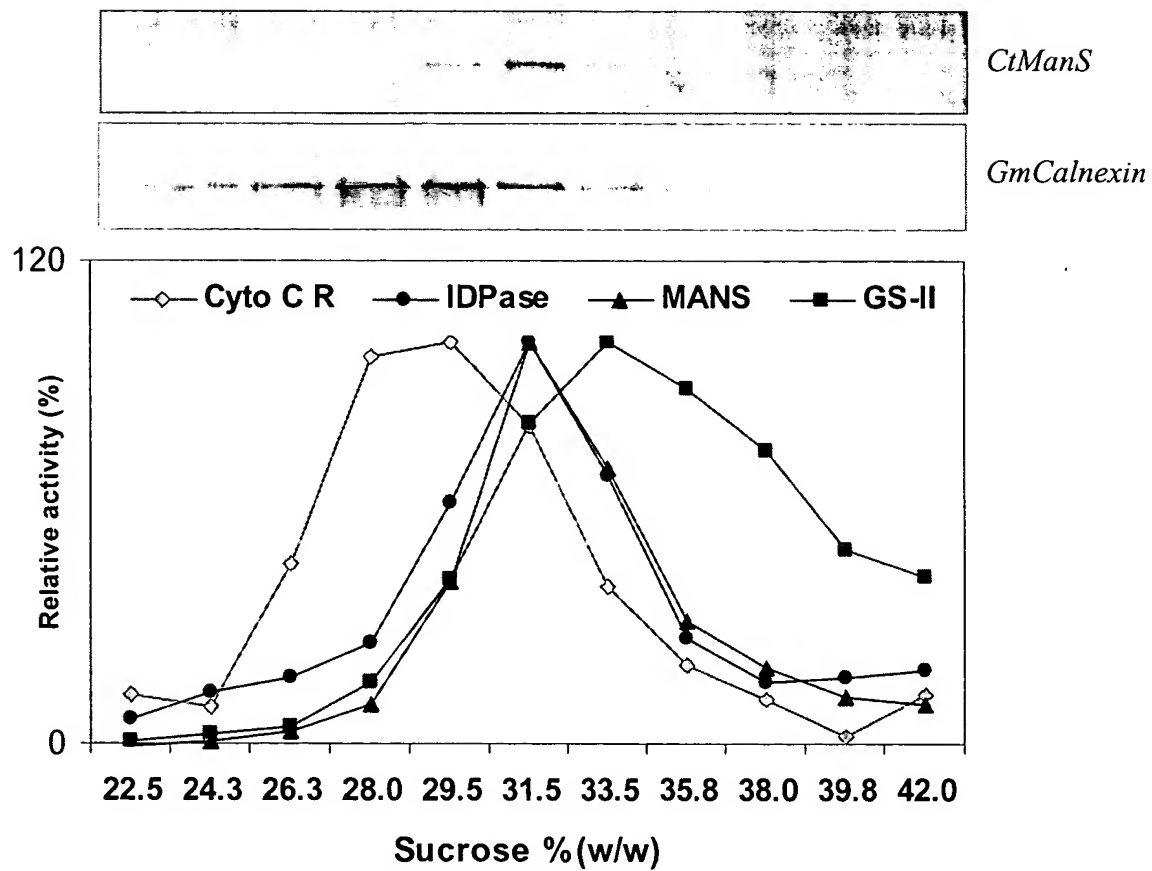


FIGURE 18

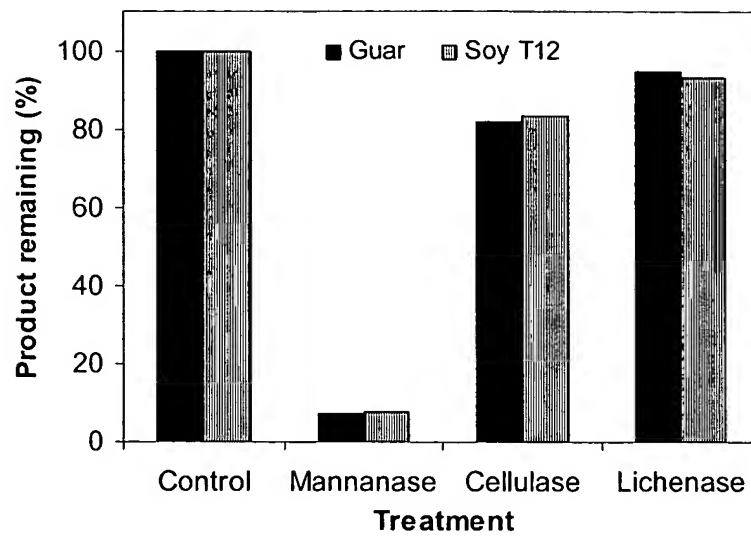


FIGURE 19

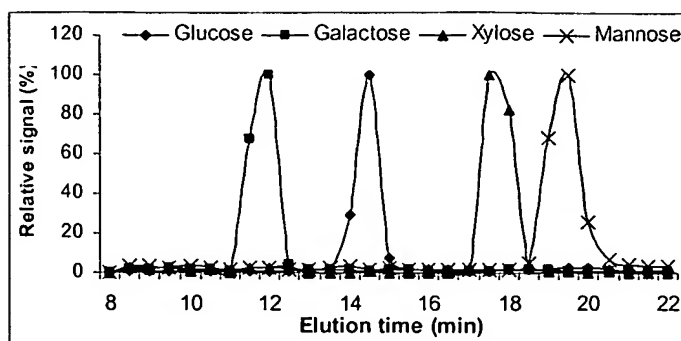


FIGURE 20A

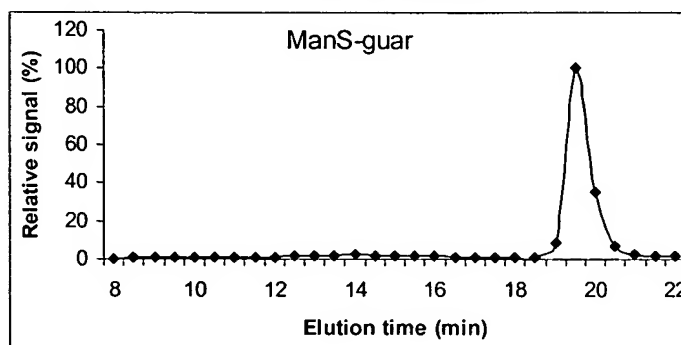


FIGURE 20B

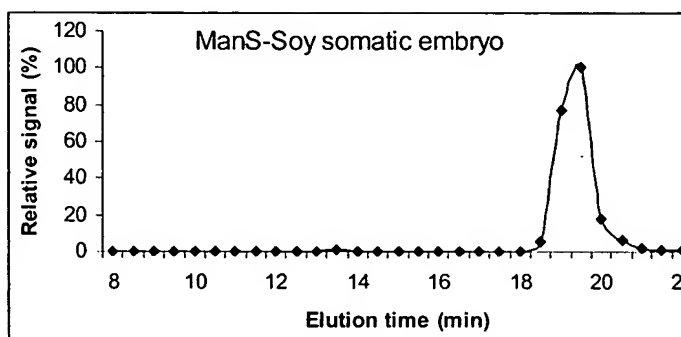


FIGURE 20C

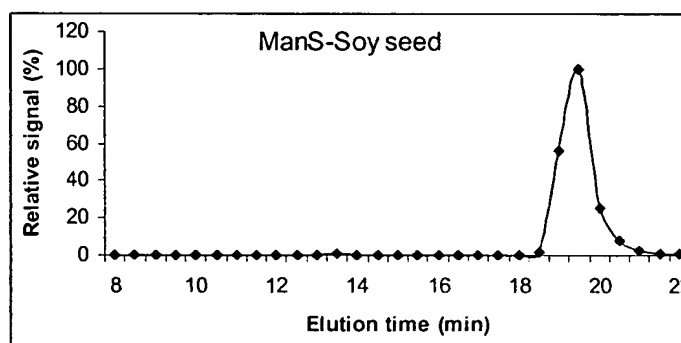


FIGURE 20D

FIGURE 20

>ClGonsT 1349 bp.

GGTGATGCAAATCGCATGAGAGGGGAAGAAGAGGTGTCTCACTTACTCTTCAATCTTCAT
TCACCCTTACGAGTGCCACCTCTCTTCTCTCCTTCTCTTACAGCTCAAACAATTTGCTG
TTAAACCTTTGATCGGTTCATCCATGGAAGAAACCTTCGTTTTCCAGTGGAGCGTTATCAG
ATCTCTCTTGTCCATCCTTCAGTGGTGGGCTTTCAATGTCACCGTTATCATCGTTAACAA
GTGGATCTTCCAGAAATTGGATTTCAAGTTTCCCCTTTCAGTATCCTGTGTACACTTTAT
CTGCTCAGCAATTGGAGCATATATCGTGATTAAGGTGCTGAAGCTTAAACCACTGATAAC
TGTTGACCCTGATGATCGCTGGAGAAGAATATTTCTATGTCATTTGTATTCTGTATTAA
CATAGTGCTGGGGAATGTGAGCCTACGGTATATTCCAGTTTCTTTTATGCAGACGATAAA
GTCATTACGCCTGCAACTACAGTTGTTCTGCAATGGCTTGTATGGAGAAAGTATTTTGA
CTGGCGTATTTGGGCTTCTCTTATTCCCATTTGTTGGAGGGATTCTTCTTACATCTGTAAC
AGAGCTTAGTTTTAATATGTTTGGATTTTGTGCTGCCTTATTTGGTTGTTTGGCCACATC
TACGAAGACTATCCTTGCAGAATCTCTTTTGCATGGATACAAATTTGATAGCATAAACAC
AGTTTACTACATGGCACCTTTGCAACCATGATCTTGGCGCTTCCTGCCATGTTACTCGA
AGGAAATGGAATTCCTTGA CTGGCTAAACACTCATCCATATCCTTGGTCAGCCCTCATCAT
TATTTTCAGCTCTGGGGTTTTGGCTTTCTGTCTCAACTTCTCCATTTTTTACGTGATTCA
CTCCACCCTGCTGTAACCTTTAACGTTGCCGGAACCTTAAGGTTGCAGTTGCTGTTCT
GGTTTCATGGCTGATATTTAGGAACCCAATATCATACTTAAATGCAGTTGGATGTGCCGT
GACACTTGTGGGATGTACATTCTATGGTTATGTAAGGCACATGCTCTCCCAACAGCCACC
AGTTCCAGGAACCTCTCGAACTCCAAGGACCCCTCGCAGTAAGATGGAGTTACTCCCTCT
TGTAATGATAAATTAGAAGATAAGGTCTAATTGTTTTAGCTATGTACACGAGGTTTATG
TCATTTCTAAGGCAGTAGTAACAGCAATATAGGTACAAAAGGATTACAGTGACTGGTTAT
TTATTCCGTTAGATTATCCCAAAATTTTCAATACAAGTTCTTTTACATTCCCTTTTTTAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 21

>CiGONST 0aa, 342 aa.

MEETFVFQWSVIRSLLSILQWWAFNVTVIIIVNKWIFQKLDFKFPLSVSCVHFICSAIGAY
IVIKVLKLKPLITVDPDDRWRRIFFPMSFVFCINIVLGNVSLRYIPVSFMQTIKSFTPATT
VVLQWLWVRKYFDWRIWASLIPIVGGILLTSVTELSFNMFGFCAALFGCLATSTKTILAE
SLLHGYKFDSINTVYYMAPFATMILALPAMLLEGNGILDWLNTHPYPPWSALIIIFSSGVL
AFCLNFSIFYVIHSTTAVTFNVAGNLKVAVAVLVSWLIFRNPISYLNAGCAVTLVGCTF
YGYVRHMLSQQPPVPGTPRTPRTPRSKMELLPLVNDKLEDKV

FIGURE 22

| | | | |
|-----------|-------|---|-----|
| | 1 | | 50 |
| CtGONST | (1) | -----MEETTFVFWQSVIR----- | |
| AtGONST5 | (1) | -----MEEGSLWRQWTMFR----- | |
| AtGONST4 | (1) | -----MSSSRFDS----- | |
| AtGONST3 | (1) | -----MSTNDEENGTVIEVKN--VPEP--SPE | |
| AtGONST2 | (1) | MSAVKLEAIVCHEPDESELSHLSNDNGSKTKNGVVFQLLDQKSSEHRWFSE | |
| AtGONST1 | (1) | -----MKLYEHDGVDLEDGKTVKSGG---DKP---IPR | |
| Consensus | (1) | MEGS ENGTVIR | |
| | 51 | | 100 |
| CtGONST | (14) | -----SLLSILQWAFNVTVIIVNKKWIF | |
| AtGONST5 | (15) | -----SLLSILQWGFNVTVIIMNKKWIF | |
| AtGONST4 | (9) | -----NKQLTSSLVIGYALCSSLAVINKLAT | |
| AtGONST3 | (24) | TWYS-----VFLRQASVYGVAAGYCLSAASLSIINKWAT | |
| AtGONST2 | (51) | RFLRWRRRYLPVDGDNRRDHGSVKQSGPLVSGAAYCISSCSMIILNKIVL | |
| AtGONST1 | (28) | KIH-----NR-----ALLSGLAYCISSCSMILVNKFVL | |
| Consensus | (51) | KQ SLLSILAYCISS SLIIINKWII | |
| | 101 | | 150 |
| CtGONST | (37) | QKLDFKFPISVSCVHFICSAIGAYIVIKVLKIKPLITVDPDDRWRRIFFPM | |
| AtGONST5 | (38) | QKLDFKFPISVSCVHFICSSIGAYIVIKVLKIKPLIVDPEDRWRRIFPM | |
| AtGONST4 | (37) | TYFNYPG--LLTALOYLCTVAVYLLGKSGLIN--HDPFTWDATAKKFLPA | |
| AtGONST3 | (58) | MKEPYPG--ALTAMOYFTSAAGVLLCAQMKLIE--HDSNLLTMRWFLPA | |
| AtGONST2 | (101) | SSYNFNAGVSLMLYQNIISCLVVAVLDISGVVS--VEKFNWKLIRVWMPV | |
| AtGONST1 | (56) | SSYNFNAGIFLMLYQNFVSVIIVVGLSLMGLIT--TEPLTLRLMKVWFV | |
| Consensus | (101) | SKFNF A LSLV VQFI SAIGVYIL KMGLI ID D MRRFFPM | |
| | 151 | | 200 |
| CtGONST | (87) | SFVFCINIVLGNVSLRYIPVSFMQTIKSFTPATTVVLQWLVWRK-VFDWR | |
| AtGONST5 | (88) | SFVFCINIVLGNISLRYIPVSFMQTIKSFTPATTVVLQWLVWRK-VFDWR | |
| AtGONST4 | (83) | AIVEYLAIFTNTNLLRHANVDTFIVFRSLTPLLVAIADTVFRSQPLPSRL | |
| AtGONST3 | (104) | AMIFYLSLFTNSELLRHANVDTFIVFRSAVPTFVAIGETLFLHQPWPSVK | |
| AtGONST2 | (149) | NVIFVGMIVSGMYSIKYINVAMVTILKNATNLLTGIGEVYMERK-RONNK | |
| AtGONST1 | (104) | NVIFVGMILITSMFSLIKYINVAMVTILKNVTNVTAVGEMYLENK-QHDNR | |
| Consensus | (151) | AVIF I IVTG SLRYINVA M VIKSLTPILTAIGE LVFRK Y D R | |
| | 201 | | 250 |
| CtGONST | (136) | IWASLPIVGGILLTSVTELSFNMFGECAALFG-----CLATSTKTIIL | |
| AtGONST5 | (137) | IWASLVPIVGGILLTSITELSFNVFGFCAALFG-----CLATSTKTIIL | |
| AtGONST4 | (133) | TELSLVVILAGAVGYVAIDSSFTLTAYSWALA-----YLVTITTEMVY | |
| AtGONST3 | (154) | TWGLSLATIFGGSLLYVFLDYQFTIAAYSWALA-----YLVSMITDFVY | |
| AtGONST2 | (198) | VWAAMFMMIISATSGGIIDLTEDAVGYTWOLANCFLTASYSLTLRRVMDK | |
| AtGONST1 | (153) | VWAALFLMIISAVSGGIIDLSFNAVGYAWQIANCFLTASYSLTLRKTMDDT | |
| Consensus | (201) | IWASLVLIIGGALL ITDLSFNI GYSWALA Y LTLST MI | |
| | 251 | | 300 |
| CtGONST | (179) | AESLLHGYKFDSENTVYYMAPFATMILALPAMLLEGNGILDWLNTHYPY- | |
| AtGONST5 | (180) | AESLLHGYKFDSENTVYYMAPFATMILGLPAFLLERNGILDWFEAHSP- | |
| AtGONST4 | (176) | IKHVMVSNIKLNIWGLVLYNNLLSLMIAPVFWFLTGEFTEVFAALSENNGN | |
| AtGONST3 | (197) | IKHVMVIGLNTWGLVLYNNLEALLFPLELLIMGELKKIKHEITDET-D | |
| AtGONST2 | (248) | AKQSTKSGSLNEVSMVLLNNLLSIPFGIILILLGEWRYMISTDVTKD-- | |
| AtGONST1 | (203) | AKQVTOSGNLNEFSMVLLNNTLSLPLGLLLSYFFNEMDYLYQTPLRL-- | |
| Consensus | (251) | AK LL S KLNSW LVLYNNLLALMIG L ALLLGE L T | |

FIGURE 23a (1 of 2)

| | | | | |
|-----------|-------|-----|---|------------|
| | | 301 | | 350 |
| CtGONST | (228) | --- | WSALIIIFSSGVLAFCLNFSIFVVIHSTTAVTFNVAGNLKVA | VAVLV |
| AtGONST5 | (229) | --- | WSALIIILFNSGVLAFCLNFSIFVVIQSTTAVTFNVAGNLKVA | VAVFV |
| AtGONST4 | (226) | | LFEPYAFSSVAASCVFGLISYFGFAARNASATAFTVTGVNKF | LTVVI |
| AtGONST3 | (246) | | WYSLOVLPVGLSCLFGLAISFFGFSCRRATISATGFTVLGIVN | KLLTVVI |
| AtGONST2 | (296) | --- | SMFWVVATASGFLGLAISFTSMWFLHQTGPTTYSLVGSLNK | VPISLA |
| AtGONST1 | (251) | --- | PSFWMVMTLSGLLGLAISFTSMWFLHQTGATTYSLVGSLNK | IPLSLA |
| Consensus | (301) | | SAWIIIV ASGVLGLAISFS FW IHATSATTFSVVG LNKIL VLI | |
| | | 351 | | 400 |
| CtGONST | (275) | | SWIIFRNPIESYINAVGCAVTLVGCTFYGYVRHMLSQQPPVP | GTPTPTPTP |
| AtGONST5 | (276) | | SWMIIFRNPISPMNAVCGITLVGCTFYGYVRHMLSQQQ-- | PSTPTPTPTP |
| AtGONST4 | (276) | | NVTIWDKHATPVGLVCLFTICGGVGYQQSVKLDKPIEKVSEK | DSEKGEE |
| AtGONST3 | (296) | | NEMWWDKHSIFVGTTEGLVCMFGGVMYQOSTEK-KPNATQE | AKPQEQDEE |
| AtGONST2 | (343) | | GLVLFNVPIESLPNLFSLFGLFAGVVFARAKMS----- | |
| AtGONST1 | (298) | | GLVLFNVPTSLONSASLFLGLVAGVVFARAKMREKS----- | |
| Consensus | (351) | | LLIF PIS VNAVGLFTLVGGVVYA AKMM K Q G P | |
| | | 401 | | 430 |
| CtGONST | (325) | | RSKMELIPLVNDKLEDKV----- | |
| AtGONST5 | (324) | | RNKMELIPLVNDKLESKIT----- | |
| AtGONST4 | (326) | | DE--ELTQLVPGKLASVV----- | |
| AtGONST3 | (345) | | QE--KLLEMQENKESNSVDIKETLKSEEKL | |
| AtGONST2 | (376) | | ----- | |
| AtGONST1 | (334) | | ----- | |
| Consensus | (401) | | ELL LV KL V | |

FIGURE 23b (2 of 2)

| | CtGONST | AtGONST5 | AtGONST4 | AtGONST3 | AtGONST2 | AtGONST1 |
|----------|---------|----------|----------|----------|----------|----------|
| CtGONST | 100 | 90 | 31 | 24 | 16 | 28 |
| AtGONST5 | | 100 | 31 | 22 | 17 | 28 |
| AtGONST4 | | | 100 | 51 | 19 | 28 |
| AtGONST3 | | | | 100 | 17 | 26 |
| AtGONST2 | | | | | 100 | 59 |
| AtGONST1 | | | | | | 100 |

FIGURE 24

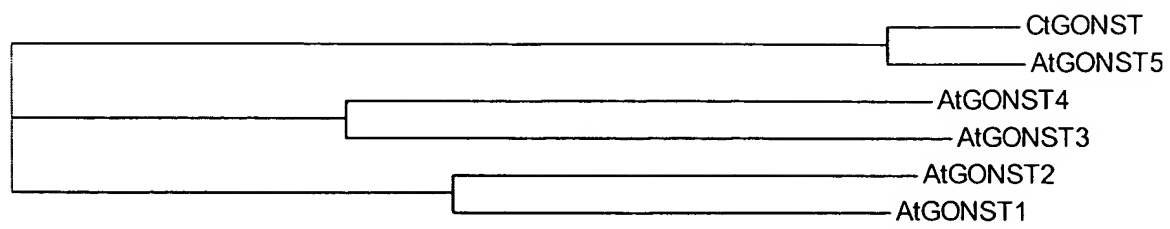


FIGURE 25

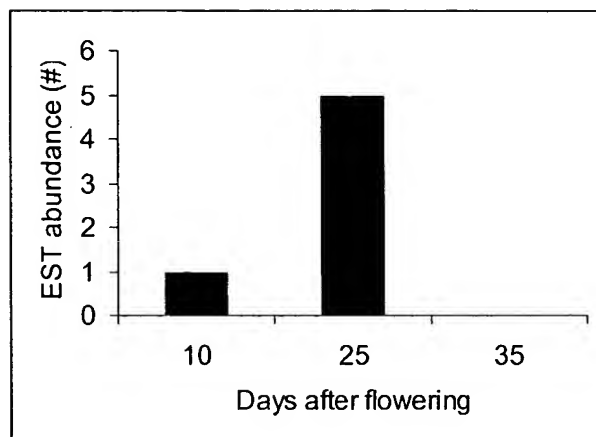
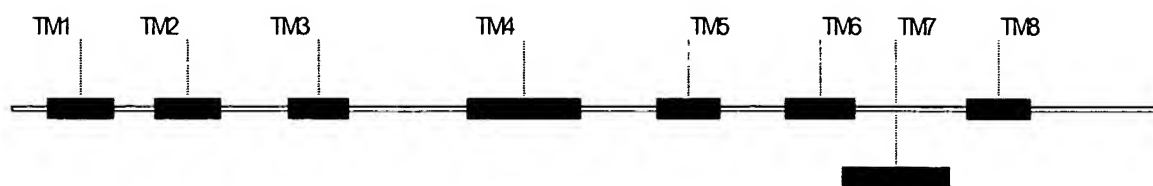


FIGURE 26



CtGONST
342 aa

FIGURE 27